rwhulb-a.rpr

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- protein search, using sw model OM protein Run on:

January 13, 2005, 15:03:32 ; Search time 33.3983 Seconds (without alignments) 3321.665 Million cell updates/sec

RWHU1B-A Title: Perfect score:

5953 1 MALRVLLLTALTLCHGFNLD......FKRQYKDMMSEGGPPGAEPQ 1153 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62DX** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 B B Minimum Maximum M Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

integrin - fruit f integrin alpha-2b	glycoprotein IIb - integrin alpha-7 c	alpha-7 integrin - leukocyte adhesion	F54F2.1 protein - integrin alpha cha	hypothetical prote	integrin alpha v c	integrin alpha cha	integrin alpha cha	glycoprotein IIb -	integrin alpha cha	integrin alpha-1 -	glycoprotein IIb -
S40311 A34269	A60163 JC5950	I61186 B30892	S44824 S38783	S28277	S60571	T09433	T09403	136916	T18523	A55348	136917
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30	332	34 35	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
RWHU1B
cell surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A; Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD1
m.
A;Reference number: A31108; MUID:88315033; PMID:2457584
A;Accession: A31108
A; Molecule type: mRNA
A;Residues: 1-1153 <cor></cor>
A; Cross-references: UNIPROT: P11215; GB:J03925; NID:g187284; PIDN: AAA59544.1; PID:g307148
A; Note: part of this sequence was confirmed by protein sequencing
R; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mc
A; Reference number: A28915; MUID: 88257215; PMID: 2454931
A:Accession: A28915

A,Accession: A28915
A,Recidues: 1-499,501-965,7P',967-1153 <ARN>
A,Residues: 1-499,501-965,7P',967-1153 <ARN>
A,Residues: 1-499,501-965,7P',967-1153 <ARN>
A,Crosa-references: GB:1418044, GB:03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA5945
A,Note: part of this sequence, including the amino end of the mature protein, was confirm R;Ballely, C.S.; Armanut, MA.

R,Shelley, C.S.; Armanut, MA.

Proc. Natl. Acad. Sci. US.A. 88, 10525-10529, 1991
A,Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regnession: A41600
A,Accession: A41600
A,Accession: A41600
A,Molecule type: DNA
A,Residues: 1-9 <SHBS
A,Crosa-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R,Armaout, MA.; Renold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. US.A. 85, 2776-2780, 1988
A,Title: molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic A;Reference number: A94193; MUD:88190151; PMID:2833753
A,Accession: A30892
A,Accession: A32218; MUD:8909893; PMID:2563162
A,Accession: A32218
A

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A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir A;Reference number: S00551; MUID:88312584; PMID:3044779 A;Accession: S00551
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                                                                                                                   SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
                                                                                                                                                                                                                  LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP
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R;Pytela, R.
EMBO J. 7, 1371-1378, 1988
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                                                                        J. Timeunol. 150, 480-490, 1993
J. Timeunol. 150, 480-490, 1993
A. Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
A;Accession: A46526
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499;Sol-1153 <- Fig. 100
A;Reference number: A90644; MUID:87076671; PMID:353920
A;Residues: 17-31 <- Fig. 100
A;Reference number: 152567; MUID:92144986; PMID:1346576
A;Recession: 152567
A;Residues: 15-870; 1992
A;Ritle: Characterization of the myeloid-specific CD11b promoter:
A;Recession: 152567
A;Residues: 15-870; 1992
A;Residues: 15-870; MUID:92144986; PMID:1346576
A;Residues: 17-870; BNA
A;Residues: 19-8785>
A;Residues: 19-8785>
A;Residues: 19-8785>
A;Residues: 10-97865
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A,NOTES: Telementes: GDB:120599; OMIM:120980
A,Map position: 16p11.2-16p11.2
A;NOTE: promoter contains a GATA motif and two Sp1 consensus binding sites
A;NOTE: promoter contains a GATA motif and two Sp1 consensus binding sites
A;NOTE: promoter contains a GATA motif and two Millebrand factor type A repeat home
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C;Keywords: alternative splicing calcium; cell adhesion; glycoprotein; heterodimer; mag
F;1-1168/Domain: satisfacts glycoprotein Dinamental cMAT>
F;17-1108/Domain: von Willebrand factor type A repeat homology cVWA2>
F;148-318/Domain: von Willebrand factor type A repeat homology cVWA2>
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted cINT>
F;115-1153/Domain: intracellular #status predicted cINT>
F;186,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
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                                                                                            the alpha-ir
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C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C;Genetics:
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Jening, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D. Immunol, 150, 480-490, 1993
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99.9%; Pred. No. 0;
ive 1; Mismatches
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Matches 1152; Conservative
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A; Residues: 1-1153 apry.

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A; Residues: 1-1153 apry.

A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983

A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983

A; Note: the authors translated the codon CAC for residue 569 as Gln

R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986

A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep A; Reference number: I59078; MUID:86287312; PMID:2942940

A; Reference number: I59078; MUID:86287312; PMID:2942940

A; Residues: Dray are allowed from GB/EMBL/DDBJ

A; Residues: 11-44 ackES

A; Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193

C; Genetics:

A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: cell surface glycoprotein transmembrane protein
C; Superfamily: cell adhesion; glycoprotein; transmembrane protein
F; 1-16/Domain: signal sequence #status predicted acid.
F; 1-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F; 148-318/Domain: von Willebrand factor type A repeat homology avwa2>
F; 1106-1129/Domain: transmembrane #status predicted aTWM>
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76.3%; Score 4542; DB 2; Length 1
Best Local Similarity. 74.4%; Pred. No. 2e-303;
Matches 859; Conservative 142; Mismatches 151; Indels
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780
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                        LSITESPMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                                                                                                                              QRSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLK
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the alpha subunit of a leukocyte

A;Gene: GDB:ITGAX; CD11C A;Cross-references: GDB:119758; OMIM:151510 A;Map position: 16p11.2-16p11.2 C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol

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Score 1556; DB 2;
Pred. No. 3.1e-98;
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34.3%;
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Best Local Similarity
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A; Residues: 1-20 <NUE>
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C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; Fi-19/Domain: signal sequence #status predicted <SIG> Fi-19/Domain: signal sequence #status predicted <SIG> Fi-20-1163/Product: cell surface glycoprotein CDIIC #status predicted <MAT> F;20-1107/Domain: extracellular #status predicted <EXT> F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4> F;149-319/Domain: transmembrane #status predicted <TMY> F;1108-1133/Domain: intracellular #status predicted <INT> F;1134-1163/Domain: intracellular #status predicted <INT> F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre
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Best Local S:
Matches 700
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cell surface glycoprotein CDlla precursor - human
NiAlternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C;0species: Homo sapiens (man)
C;0steces: Homo sapiens (man)
A;1stecence number: S03308; A47458; A48759; S36044
A;Reference number: S03308; MUID:89139587; PMID:2537322
A;Reference number: S03308; MUID:89139587; PMID:2537322
A;Reference number: S03308; MUID:89139587; PMID:2537322
A;References: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CDA687;
A;Resiques: 1-1170 claR>
A;Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CDA687;
A;Accession: A47458; MUID:39248261; PMID:8097887
A;Reference number: A47458; MUID:93248261; PMID:8097887
A;Residues: 1-20 cCOR>
A;
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A;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A : C;Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface an F;1-25/Domain: signal sequence #status predicted <SIG>F;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status F;154-317/Domain: von Willebrand factor type A repeat homology <WA2>
                                                   ENNMPRINKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
                                                                                                                                                                                          RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                                                                                                                   | ||:|: | || || || :: | :: | ||::| ||::| RDLPVSINFWVPVELNQEAVWMDVEVSHPQNPSLRCSSEKIAPPASDFLAHIQKNPVLDC
                                                                                                                                                                                                                                                                                                                                                                                          SIAVÇQRIQCDIPFRGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGQGAFVRSQTETKVEPFEVPNPLPL1VGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
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A, Rosaldus: 1-20 <SHE>
A, Cross-references: 1-20 <SHE>
B, Cross-references: 1-20 <SHE>
B, Nucda, A.; Lopes-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 268, 13305-19311, 1993
A; Title: Characterization of the CD1a (alphal, LFA-lalpha)
A; Reference number: A48759; MUID: 93374910; PMID: 8103515
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Length 1170;

OY 1040 IQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSGTFTKVE 1099    :	RESULT 5 156126 1ymphocyte fuction-associated molecule-1-alpha - mouse C;Species: Mus musculus (house mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: 156126 R;Kaufmann, Y; Teenq, E.; Springer, T.A.	J. Immunol. 147, 369-374, 1991 A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit A;Reference number: 156126; MUID:91268576; PMID:2051027 A;Accession: 156126 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule types: mRNA A;Molecule types: mRNA A;Residues: 1-1163 <res></res>	A;Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786 C;Genetics: A;Genetics: A;Guperfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol F;151-315/Domain: von Willebrand factor type A repeat homology <vwal></vwal>	Query Match 26.0%; Score 1546; DB 2; Length 1163; Best Local Similarity 34.1%; Pred. No. 1.5e-97; Matches 408; Conservative 217; Mismatches 464; Indels 106; Gaps 38;	Qy 1 MALRVLLLTALTLCHGFNLDTENAMTFQENA-RGFGQSVVQLQGSRVVVGAPQ 52	Qy 53 EIVAANQRGSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQT 112	QY 113 CSENIYYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEF 172	Qy 173 VSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEF-QNNPNPRSLVKPITQLGRTHTATGI 231	OY 232 RKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYBDVIPEADREGVIRYV 284	OY 285 IGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKKFAIEGTQTGSSS 344	QY 345 SFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDWNDAX 403	QY 404 LGYAAA-IILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGGAYFGAS 460	OY 461 LCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEGGQPWGR 520	Oy 521 FGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR 580
Matches 409; Conservative 211; Mismatches 464; Indels 110; Gaps 38;  6 LilitalitachGFNidtenamico-enagegosvologskvvgapoel 54	115 ENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMK	231 IRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA 290  237 INVVATEVFREELGARPDATKVLIITDGEATDSGNIDAAKDIIRYIIGIGKH 289  291 FRSEKSRGELNTIASKPRDHVFQNNFFALKTIONQLREKXFAIEGTQTGSSSSFEHEM 350	290 FQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKIYVIEGTSKQDLTSFNWEL 349 351 SQEGFSAAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINWTRVDSDWNDAYLGYAAA 409           :	410 -IILRNRVQSLVLGAPRXQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDV 466 :   :	467 DSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAA 524	525 LTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSGRIAGSKLSPRLQYF 584	585 GGSLSGGODLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV 644	645 -KGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKUSTRQT 703	704 QVLGLTQTCETLKLQLPNCIEDFVSPIVLRLNFSLVGTPLSAFGNLRPVL 753 	754 AEDAQRLFTALPPFEKNCGNDNICQDDLSITFSFWSLDCLVVGGPREFNVTVTVRNJGED 813 1	814 SYRTQVTPFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKGTSCSINHPI 871	872 PPENSEVTENITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLELPVKXAVY 927	928 MVVTSHQVSTKYINFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFLVPVRLNQTVI 983 :::           ::         ::	984 WDRPQYTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFG 1039 :

::	QTCSENTYVKGLCFLFGSNLRQQPQ	11/ SLSSELTGTCSLLGPDLKPQAQANFFDLENLLDPDARVDTGDCYSNKEGGGEDDVNT 173 136 -KFPRALRGPORDSDIAFLINGSGSTIPHDRPRMKREVSTVMRD1. 180		181 -KKSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELF 239	EKCFECNFALVQYGGVIQTEFDLRDSQDVMASLARVQNITQVGSVTKTASAMQHVLDSIF	240 NITNOARKNAPKILVVITDGEKFGPDLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQE 299  1.	LINTIASKPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAI	354 LNLIASDPDETHAFKVTNYMALDGLLSKLRYNIISMEGTVGDALHYQLAQIGFSAQI 410	TSNGP-LLSTVGSYDWAGGVFLY-TSKEKSTFINMTRVDSDMNDAYLGYAAAIILR	411 LDERROVLLGAVGAFDWSGGALLYDTRSRRGRFLNQTAAAAADAEAAQYSYLGYAVAVLHK 470 414 NRVQSLVLGAPRYQHIGLVAMFR-QNTGMWESNANV-KGTQIGAYFGASLCSVDVDSNGS 471	471 TCSLSYVAGAPQYKHHGAVFBLQKEGREASFLPVLEGEQMGSYFGSELCPVDIDMDGS 528	TDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDV	IDFLLVAAPFYHVHGEEGRVYVXRLSSE-QDGSFSLARILSGHPGFTNARFGFAMAAMGDL	532 NGALLIUVALIGYETT - GEBLUKT - GYLLEHGISCSGISESKISKILGYKUGYKG 585 	QSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVK	64./ MSPMAGGFULSGUGLADITYGTLGQAYVFRSKPYVRLKVSMAFTPSALPIG 696	FNGVNVRLCFEI-SSVTTASESGLREALLNFTLDVDVGKQRRRLQCSDVRSCLGCLREW	706 LGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLF 761	TALFPERNCGNDNICODDLSITFSFMSLDCLVVGGFREFNVTVTVRNDGEDSYRTQVTF	814 IFQLPYEKACKNKLFCVAELQLA-TTVSQQELVVGLTKELTLNINLTNSGEDSYMTSMAL 872	822 FFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFN 881 :	882 ITFDVDSKASLGNKLLLKANVISENNMPRTNKTEFQLELPVKYAVYMVVISHG 934	923 VVWQLEENAFPNRTADITVTVTNSNERRSLANSTHTLQFRHGFVAVLSKPSIMYVNTGQG 982	935 VSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFS 992 :	993 BNLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEFNATLKGNL 1052     :     :     :     :	SPDWYIKTSHNHLLIVSTAEILENDSVFTLLPGQGAFVRSQTETKVEPFEVPNP 
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		989		Db 694 SGNTSITP-DKSCLDFHFHFPICIQDLISPINVSLNFSLLEEEGTPRDQKGRAMQPILRP 752	CLVVGGPREFNVTVTNRN	810	DD 805 SGEDAYWYRLDLDFPRGLSFRKVEMLQPHSRMPVSCEELTEGSSLLTKTLKCNVS 859	QY 869 HPIFPENSEVTENITFDVDSKASLGNKLLLKANVTSEN-NMPRINKTEFQLELFVKYAVY 927			988		1022 - FWRITION-CAMPICATE TAXAS CONTINUED TO CONTINUE VIOLATION CONTINUE VIOLAT	1099 EPFEVENPLPLIJUGSSVGGGLIALITAALYKLGFFKQYKDNM-SEGGPPGAEP 1152	Db 1078 DLIHEKEMLHVYVLSGIGGLVLLFLIFLALYKVGFFKRNLKEKMEADGGVPNGSP 1132	RESULT 6 A53213		C.Accession: A53213 R.Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M. J. Biol. Chem. 269, 6016-6025, 1994	A.Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un A.Reference number: A53213, MUID:94164962; PMID:8119947 A.Accession. A53213	A/Status: preliminary A/Molecule type: mRNA	A; Residues: 1-1179 <sha> A; Cross-references: UNIPROT: P38570; GB: L25851; NID: g457244; PID: g457245 C; denetics:</sha>	Ajene: GDB:ITGAE AjCrose-rese: GDB:330801 AjMan nogitjen: 17513	Arian postramily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home F:199-371/Domain: von Willebrand factor type A repeat homology <vwa3></vwa3>	ilarity 28.7%; Pred. No. 5.1e-71;	0	ÖVARPWLTPKGGAPFVLSSLLHQDPSTNQTWLL'√T CEPI-RLQVPVEAVNMSLGLSLAATTSPP

CY 631 EVARNVFECNDQVVKGKEAGEVRVCLHVQ-KSTRDRLREGQIQSVVTYDLALDSGRPH 687		RESULT 8  RESULT 8  Integrin alpha 2 subunit - bovine (fragment)  C; Species: Bos primigenius taurus (cattle)  C; Accession: 145314  A; Fametar 1: Parada, Y.  J. Biol. Chem. 269, 9659-9663, 1994  A; File: Identification of putative ligand binding sites within the I-domain of integrin A; Reference number: A54402; MUID: 94193647; PMID: 7511592  A; Accession: 145314  A; Status: Prelimary; translated from GB/EMBL/DDBJ  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Status: preliminary; translated from GB/EMBL/DDBJ  A; Status: preliminary; A; Societion: Cattle A; Status: Parada homology cVWA2>  A; Coss-references: UNIRFORT: PS3710; GB: L25886; NID: 9439695; PIDN: AABS9255: 1; PID: 9439696  Cuery Match  A; Coss-references: UNIRFORT: PS3710; GB: L25886; NID: 949695; PIDN: AABS9255: 1; PID: 9439696  Cuery Match  Best Local Similarity 27.8%; Pred: No. 1.3e-66; Matches 339; Conservative 216; Mismatches 498; Indels 168; Gaps 47;  Cy  C; DysrdsCREPIRLOVVVEANWRIGHSINATSPPOLIACGPTWHOTICSBY 117  Db  73 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Db  73 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Cy  74 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Cy  75 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Cy  76 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Cy  77 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  Cy  78 PVDLSTTCEKLNIGTSTSMSNVTEWKINMSLGISLAATTSPPOLIACGPTWHOTICSBY 117  CHILL
Db 1073 SWDHSELLKDVTELQILGEISFNKSLYEGLNAENHRTKITVVFLKDERYHS 1124  Qy 1107 LPLIVGSSVGGLLLLALITAALYKLGFFKRQXKDWMSE 1144	RESULT 7  A45226 Cincegrin alpha-1 chain - human (fragment) Cipace: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 Cipacesion A6226 Airitle: Expression of native and truncated forms of the human integrin alpha 1 sul A;Reference number: A4526; MUID:93155124; PMID:8428973 Airitle: Expression of native and truncated forms of the human integrin alpha 1 sul A;Reference number: A4526; MUID:93155124; PMID:8428973 Airitle: Expression of native and truncated forms of the human integrin alpha 1 sul A;Residues: 1-1151 ABIN A;Resid	0

, qa	133 YTTGV	YTTGVCSDVSPDF-QLRTSFAPAVQTCP-SFIDVVVVCDESNSIYPWDAVKNFLEKFV 188
ò	178 EQLK-	-KSKTLFSLMQYSEBFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGI 231
DP	189 GGLDIC	GLDIGPTKTQMGLIQYANNPRVVFNLNTFKSKDEMIKATSQTFQYGGDLTNTFKAI 245
70	232 RKVVRI	RKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGV 287
ОЪ	246 QYARD	: QYARDTAYSTAAGGRPGATKVMVVVTDGESH-DGSKLKAVIDQCNKDNILRFGIAVLGYL 304
δλ	288 -GDAFI	GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKKFAIEGTQTGSSSSF 346
Op	305 NRNALI	· Z
δλ	347 EHEMS(	EHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMN-D 401
Dp	364 QMEMS(	OVGFSAEYSPQNNILMLGAVGAYDWSGTVVQKTPHGHLIFSKQAFEQILQDRNHS 423
λ̈	402 AYLGY	AAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGA 455
Dβ	424 SYLGYS	
λ̈	456 YFGASI	CCSUDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGE 513
Db	479 YFGSVI	
à	514 QGQPWC	QGQPWGRFGAALIVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIA 573
Dp	536 NGLEN	ARFGSAIAALSDINMDGFNDVIVGSPLENQNSGAVYIYNGHEGM-IRLRYSQKIL 594
٥y	574 GSKI	LSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPRE 631
ΩÞ	ä	AFSSHLQYFGRSLDGYGDLNGDSITDVSVGAFGQVVQLWSQSIADVSVDASFTPKK 654
ολ	632 VARNVE	FECINDOVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPH 687
Dβ	655 ITLI	ITLINKNAEIKLKLCFSAKFRPTNQNNQVAIVYNITIDEDQFSSRVI 701
δ	688 SRAVE	SRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPL 743
Db	702 SRGLF	RGLFKENNERCLQKTMIVSQAQRCSEYIIHIQEPSDIISPLNLCMNISLENPGT 756
ò	744 SAFGNLR	RPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPR 799
Db	757	-NPALEAYSETVKVFSIPFHKDCGDDGVCISDLVLNVQQLPATQQQPFIVSNQNK 810
<i>ا</i> م	800 EFNVT	FNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSG 858
οp	811 RLTFS	QLKNKKESAYNTEIVVDFSENLFFASWSMPVDGTEVTCQIAS 858
٥'n	859 ALKSTE	ALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQL 918
οgo	859 SQKSVI	QKSVTCNVGYPALKSKQQVTFTINFDFNLQ-NLQNQASISFRALSESQEENMADNSVNL 917
λo	919 ELPVKY	~
qq	918 KLSLLY	FIFSIKVTTGSVP
δ	969 SLVFLV	SLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKE
QQ	974 SMA	SVIIHIPQYTKDKNPLMYLTGVHTDQAGDISCEABINPLKIGQTSSSV 1024
ò	1010 DFLAE-	DFLAE-LRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIV 1068
qq	1025 SFKSEN	FRHIKELNCRTASCSNIMCWLRDLQVKGEYFLNVSTRIWNGTFAASTFQTVQLT 1084
 %	1069 STAEI-	-LENDSVFTLLPGQGAFVRSQTETKVEPFE-VPNPLPLIVGSSVGGLLL 1120
 업	1085 AAAEID	AAABIDTYNPQIYVIBENTVTIPLTIMKPHEKVBVPTGVIVGSVIAGILL 1134
 &	1121 LALITA	LALITAALYKIGFFKRQYKDM 1141
q <sub>0</sub> ,	1135 LLALVA	LALVAILWKLGPFKRKYEKM 1155

VIA-2 protein homolog - mouse C;Species: Mus musculus (house mouse) C;Becies: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004 C;Accession: S44142 R;Bedlama, J.M.; Chan, B.M.; Unival, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latze: submitted to the EMBL Data Library, January 1994 A;Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not v A;Reference number: S44142 A;Accession: S44142 A;Accession: S44142 A;Status: preliminary A;Rolecule type: mRUNA A;Residues: 1-1178 <EDB-A;Residues: 1-1178 <EDB-A;Cross-references: UNIPROT: Q62469; EMBL: Z29987; NID: 9473098; PIDN: CAA82877.1; PID: 9473098; F;169-344/Domain: von Willebrand factor type A repeat homology <VWA2> 168 569 135 QCGNQYXATGIC----SDVSPDFQFLTSFSPAVQACPSL-VDVVVVCDESNSIYP---WEA 187 286 GV-----GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQT 340 307 AVLGYLNRNALDTKNLIKEIKAIASTPTERYFFNVADEAALLEKAGTLGEQIFSIEGTVQ 366 426 ODRNHSSFLGYSVAAISTEDGVHFVAGAPRANYTGOIVLYSVNK---OGNVTVIOSHRGD 482 483 QIGSYPGSVLCSVDVDXDTITDVLLVGAPTYMNDLKKEEGKVYLPTITKGILNQHQ---F 539 GSLYQC--DYSTGSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQ 111 169 MKEFVSTVMEQLK--KSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLG-RT 225 226 HTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVI 285 GSSSSFEHEMSQEGFSA--AITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVD 396 SDMN-DAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGT 451 QIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTR--GGOVSVCPLPRGQRARWQCDAV 509 540 LEGPEGTGNARFGSALAALSDINMDGFNDVIVGSPVENENSGAVYIYNGHQGT-IRTKYS 598 570 QRIAGSKLSPR--LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEF 627 658 683 TP------DKITILINKDAKITIKLCFRAEFRPAGQNNQV--AILFNMTLDADGHS 705 684 GRPHSRAVFNETKNSTRRQTQVLGLTQTCET--LKLQLPNCIEDPVSPIVLRLNFSLVGT 741 9 74 5 VLLLTALTLCHGFNLDTENAMTFQ-ENARGFGQSVVQL---QGSRVVVGAPQEIVAANQR 112 TCSENTYVKGLCFLPGSNLRQQPQ---KFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRR LYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHS 628 NPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----S Indels 188; Length 1178; Query Match
18.2%; Score 1086; DB 2; 1
Best Local Similarity 28.1%; Pred. No. 6.2e-66;
Matches 347; Conservative 210; Mismatches 492; 510 61 341 397 452 g ద ò g В 원 장 Ωp ò ò ò à 셤 Š ò g. ò q g q ò qq 8 g ò

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00	706 SRVTSRGVFRENSERFLQXNMVVNEVQKCSEHHISIQKPSDVVNPLDLRVDISLENP 762  742 PLSAFGNLRPVLAEDAQRLFTALPPFEKNCGNDNICQDDLSIFPSFMSLDC 792  763 GTSPALBAYSETVKVPSIPPYKECGSDGICISDLILDVQQLPAIQTQSF 811	F;1-29/Domain: signal sequence #status predicted <sig> F;30-1133/Domain: extracellular #status predicted <ext> F;172-347/Domain: von Millebrand factor type A repeat homology <vwa2> F;1724-1154-1154/Domain: transmembrane #status predicted <tyma> F;1155-1181/Domain: intracellular #status predicted <cyt> F;105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)</cyt></tyma></vwa2></ext></sig>
	DVGGFEET V TVRNOGES TO THE FFEED STANDARD STANDA	Query Match 18.2%; Score 1084.5; DB 2; Length 1181; Best Local Similarity 27.2%; Pred. No. 7.9e-66; Matches 338; Conservative 215; Mismatches 498; Indels 193; Gaps 44;
	ST-EVGGALKETSCSINHPIFFENSEVTENITFOVDSKASLGNKLLLKANVISENNMFKT         :     :     :       :	Qy 3 LRVLLLTALTLCHGFNLDTENAMTFQ-ENARGFGQSVVQLQGSRVVVGAPQE 53
6 40 Pp 6	912 NKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR 964 	Qy 54 IVAANQRGSLYQCDYSTGSCEPIRLQVPVEAVMNSLGLSLAATTSPPQLLA 104
	SLPISLVFLVPVRLNQTVIND	Qy 105 CGPTVHQTCSENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQBDSDIAFLIDGSGSIIPH 164  Db 131 CGPLWAQQCGNQYYTTGVCSDISPDF-QLSASFSPATQPCFSL-IDVVVVCDESNSIYPW 188
		Qy 165 DFRRMKEFVSTVMEQLKKSKTLFSLMQYSBEFRIHFTFKBFQNNPNPRSLVKPITQLL 222
		Qy 223 G-RTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVI 281
9y Bb 11	1105	Qy 282 RYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKKFAIE 336  GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKKFAIE 336
RESULT 10 A33998 integrin al N;Alternate C;Species: C;Date: 30-	RESULT 10 A33998 integrin alpha-2 chain precursor - human N;Alternate names: CD499; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2 ch C;Species: Homo sapiens (ma) C;Date: 30-Mar-1990 #sequence revision 18-Sep-1992 #text_change 09-Jul-2004 C;Accession: A33999; B56793; Ā53117	QY         33.7 GTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT- 393           DD         36 GTVQG-GDNFQMEMSQVGFSADYSSQNDILMLGAVGAFGWSGTIVQKTSHGHLIFPKQAF 424           QY         394 -RVDSDMN-DAXLGYAAAIILRNRVQSLVLGAAPRYQHIGLVAMFRQNTGMMESNANV 448           DD         425 DQILQDRNHSSYLGSYSAAISTGESTHFVAGAPRANYTGQIVLYSVNENGNITVI 479
R; Takada, 1 J. Cell Bic A; Title: Th A; Reference	Y.; HemLer, M.E. he primary structure of the VLA-2/collagen receptor alpha(2)-subunit (platelet e primary structure of the VIA-2/collagen receptor alpha(2)-subunit (platelet e primoper: A33998; MUID:89308879; PMID:2545729	Qy 449KGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRAR 503
A; Molecule A; Residues: A; Cross-ref	907	OY 504 WQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSG 563
A; Note: the R; Catimel, Biochem. J. A; Title: Se	e authors translated the codon GAI for residue 802 as GIN, GFC for residue 803 B.; Parmentier, S.; Leung, L.L.; McGregor, J.L 279, 419-425, 1991  eparation of important new platelet glycoproteins (GPIa, GPIc, GPIc*, GPIIa an	Qy 564 ISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQPVLRV 621   :
A; Reference A; Accession A; Molecule A; Residues:	e number: A56793; MUID:92061944; PMID:1953640 n: B56793 type: protein : 30-43 <cat></cat>	Qy 622 KAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLAL 681  Db 656 AIEASFTPEKI TLVNKNAQIILKLCFSAKFRFTKQNNQVALVYNITL 702
A; Experimen R; Zutter, P J. Biol. C! A; Title: T:	ntal Bource: platelet M., Santoro, S.A.; Painter, A.S.; Tsung, Y.L.; Gafford, A. hem. 269, 463-469, 1994 he human alpha-2 integrin gene promoter. Identification of positive and negati	Qy 682 DSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSBIVLRLN 735
A; Kererence A; Accession A; Molecule A; Residues:	number: A5311/; MUID:94103255; FMID:82/6836 n: A53117 type: DNA : 1-16,'V',18-21 <zut></zut>	Qy 736 FSLVGTPLSAFGNLRFVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLD 791
A;Cross-re. A;Note: au C;Genetics A;Gene: GDE	A;Cross-references: GB:L24121; NID:9400342; PIDN:AAA16619.2; PID:94583535 A. A;Note: authors translated the codon GTA for residue 17 as Leu C;Genetics: CD8:ITGA2; CD498	Qy 792 CLUVGGPREFNUTVIVRNDGEDSYRTQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESA 851 :
A; Cross-re, A; Map posit C; Keywords	A,Cross-references: GDB:128031; OMIM:192974 A;Map position: 5g11.1-5g11.2 C;Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein	Qy 852 SST-EVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFR 910

QY 402AYLGYAAAIILRNRYQSLYLGAPRYQHIGIVAMFRONTGMWESNANVKGTQIGAYFG 458 -	Db 610 KTIREAYAQRIPSGGDGKTLKFFGQSIHGEMDLNGDGLTDVTIGGIGALFWARDVAVV 669  Qy 622 KAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQ-KSTRDRLREGQIQSVVTYD 678  Db 670 KVTWNFEPNKVNIQKRCRVBGKETVCINATMCFHVKLKSKEDSIYEADLQYR 722  Qy 679 LALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCI 723  T3 VTLDSLRQISRSFFSGTQERKIQRNITVRESECIRHSFYMLDK 765	724 EDPUSPIULEINFSLUGTPLSAFGNIRPULAEDAQRILFTALFPERNCGNDNICQDDLSI	Oy 988OVTESEMISSTCHTKERLPSHSDFLAELERAPVINOSIAV 1027	RESULT 12 A41131  Jymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse N;Alternate names: integrin alpha-4 N;Alternate names: integrin alpha-4 C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Accession: A41131; S16/42 R;Nuchaus; H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzmann, B.; Weissman, I.L. J; Cell Biol. 115, 1149-1158, 1991 A;Title: Cloning and expression of cDNAs for the alpha subunit of the murine lymph A;Reference number: A41131; MUID:92064645; PMID:1840602
Db 862 EVTCQVAASQKSVACDVGYPALKREQQVTFTINFDFNLQ-NLQNQASLSFQALSESQEEN 920  Qy 911 TINKTEFQLELPVKYAVYMVTSHGVSTKXLNFTASENTSRVMQHQYQVSNLGQR 964	Qy         1046 ATLKGNLSFDWYIKTSHNHLLIVSTABI-LFNDSVFTLLPGQGAFVRSQTETKVEPFEVP 1104           Db         1073 VNVTTRIWNGTFASSTFQTVQLTAAABINTYNPBITVIEDNTVTIPLMIM 1122           Qy         1105 NPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDM 1141           Db         1123 KPDEKAEVPTGVIIGSIIAGILLLALITAALWILWKLGFFKRKYEKM 1166           RESULT 11	A35854  A35854  A169rin alpha-1 chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004 C;Accession: A35864; S1123 C;Accession: A35854 A;Tignatius, M.J; Large, T.H; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, J. Cell Biol. 111, 709-720, 1990 A;Tifle: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin a A;Reference number: A35854 A;Reference number: A35854 A;Reference number: A35854 A;Residues: Preliminary A;Molecule type: mRNA A;Residues: 1-180 < IGN> A;Cross-references: UNIPROT:P18614; GB:X52140; NID:956493; PIDN:CAA36384.1; PID:956494 C;Keywords: cell adhesion; cytoskeleton; transmembrane protein F;170-345/Domain: von Willebrand factor type A repeat homology <vwa2> Query Match Best Local Similarity 27.6%; Pred. No. 1.9e-65; Matches 350; Conservative 200; Mismatches 484; Indels 234; Gaps 47;</vwa2>	Qy 6 LLLTALTLCHGFNLDTENAMTFQENARG-FGQSVVQLQGSRVVVGAPQEIVAANQRG 61  18 LLTVILGFCVSFNVDVKNSMSFSGPVEDMFGYTVQQYENEGKWVLIGSPLVGQPKARTG 77  Qy 62 SLYQCDYSTGSCEP-IRLQVPVEAVNMSLGLSLAATTSPPQLLACGFTVHQ 111  78 DVYKCPVGRERAMFCVKLDLPVNTSIKENMTFGSTL-VTNPNGGFLACGFTVHQ 111  78 DVYKCPVGRERAMFCVKLDLPVNTSIFNMTFGSTL-VTNPNGGFLACGFTYNQ 136  Qy 112 TCSENTYVKGLCFLFGSNLRQOPQKFPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKE 171  Db 113 RCGHLHYTTGLSDVSPTFGVVNSFAPVQECSTQ-LDIVIVLDGSNSIYPWESVIR 191  QY 172 FVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFRFQNNPNPRSLVKDTTQLLG-RTHTA 228	Qy 229 TGIRKUVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVG 288  bb 252 LGIDTARKEAFTEARGARRGVKKVMVIVTDGESH-DNYRLKQVIQDCEDENIQRFSIAIL 310  QY 289 DAFRSEKSROBLNITASKPPRDHVFQVNNFEALKTIQNQLREKKFAIEGTQTGSS 343  11 GHYNRGNLSTEKFVEBIKSIASEPTEKHFFNVSDELALVTIVKALGERIFALEATADQSA 370  QY 344 SSFEHEMSQEGFSAAITSNGPLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMND 401

lymphocyte-1

1.L.

A,Status: A,Molecule A,Residues A,Cross-re C,Superfar C,Keywords Query Ms Best Loc Matches Qy Db Db	A; Status: preliminary A; Molecule type: mRNA A; Casedidues: 1-1039 acutus C; Superfamily: integrin alpha-4 chain Matches 284; Conservative 190; Mismatches 412; Indels 368; Gaps 48; Cy 2 ALRVILLTALTICHGENIDTENAMICO-ENARGEGOSY-OLOGGSRVVVGAPQEIVA 57 Cy 2 ALRVILLTALTICHGENIDTENAMICO-ENARGEGOSY-OLOGGSRVVVGAPQEIVA 57 C;	Db 706 BVTESSGIVK-LACSLGYIYVDRLSRIDISFLLDVSSLSRAHEDLSISVHASCENEG 761  Qy 907 NMPRTNKTEPQLELPVKYAVYMVYTSHGVSTKYLNFTASENTSRVMQHQYQVS 959  1
8 4 8 4 8 4 8 6 8	GSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFGNNFNPRSLVK	RESULT 13 S06046 integrin alpha-4 chain precursor - human NyAlternate names: CD494; very late antigen-4 alpha chain; VLA-4 alpha chain C;Species: Homo sapiens (man) C;Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004 C;Accession: S06046; A39355; D28018 R;Takda, Y; Elices, M.J; Crouse, C.; Hemler, M.E. EMBO J. 8, 1361-1368, 1989 A;Title: The primary structure of the alpha(4) subunit of VLA-4: homology to other integrance of muber: S06046; MUID:89356603; PMID:2788572 A;Accession: S06046 A;Molecule type: mRNA A;Resenion: S06046 A;Accession: MARNA A;Resenion: G.; Birkenmeier, T.M.; Dean, D.C. Proc. Natl. Acad. Sci. U.S.A. 88, 4094-4098, 1991 A;Title: Characterization of the alpha-4 integrin gene promoter. A;Reference number: A39355; MUID:91239513; PMID:2034655
8 8 8 8 8 8	449 KGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRA-RWQCD 507	A; Molecule type: DNA A; Residues: 1-93 < ROS> A; Residues: 1-93 < ROS> A; Residues: 1-93 < ROS> A; Cross-references: GB: M62841 R; Takada, Y.; Strominger, J.L.; Hemler, M.E. Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987 A; Title: The Very late antigen family of heterodimers is part of a superfamily of molecul A; Reference number: A94151; MUID: 87204112; PMID: 3033641 A; Residues: A0-50, E', 52-53 < TA2> C; Genetics: Assidues: A0-50, E', 52-53 < TA2> C; Genetics: A; Cross-references GDB: 128032; OMIM: 192975 A; Cross-references GDB: 128032; OMIM: 192975 A; Map position: 2931-2932
6 6 6 6 6 6 6 6	481 S-HPESVNÄTKEDČTENĞIPSVÇMİLTLCFSYKGKEVPGYIVLEYNVSİDVHR 532 686PHSRAVFNETKNSTRRQTQVLGLTQCETLKLQLENCIEDPVSPIVLRINFSL 738 533 KAESPERFYFESNGTSDVITGSIRVSSGEKCRTHQAFMRKDVRDILTPIHVEATYHLGH 592 739VGTPLSAFGNLRPVLAEDAQR-LFTALFPFEKNGGNDNICQDDLSITFSFM 788 739VGTPLSAFGNLRPVLAEDAQR-LFTALFPFEKNGGNDNICQDDLSITFSFM 788 739VGTPLSAFGNLRPVLAEDAQR-LFTALFPFEKNGGNDICQDDLSITFSFM 788 739CGTPLSAFGNLRPVLAEDAQR-LFTALFPFEKNGTAYRSFM 788 739CGTPLSAFGNLRPVLAEDAQR-LFTALFFFELDLSYRKVSTLQNQRSQRSWRLAC 848, 593 HVITKRNITEEFPPLQPILQQKKEKDVIRKMINFAFFFLDLSYRKVSTLQNQRSQRSWRLAC 848, 652 NKTYLAVGGNRFTIMLNVSLFRAGDDAYETTLNVQLFTGLYFIKILDLEKQINC 705 849 ESASSTEVGGALKSTGSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLIKANNTSEN 906 849 ESASSTEVGGALKSTGSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLIKANNTSEN 906	C;Superfamily: integrin alpha-4 chain C;Superfamily: integrin alpha-4 chain C;Keywords: cell adhesion; cytoskeleton; duplication; glycoprotein; heterodimer; transmen C;Keywords: cell adhesion; cytoskeleton; predicted <sig> F;1-39/Domain: signal sequence #status predicted <sig> F;40-1038/Product: integrin VLA-4 alpha-4 chain #status predicted <mat>  Query Match  10.7%; Score 639; DB 2; Length 1038; Best Local Similarity 23.9%; Pred. No. 2.6e-35; Matches 298; Conservative 174; Mismatches 417; Indels 358; Gaps 53;  Qy  S VILLTALTLCHGFNIDTENAMTFQ-ENARGFGQSVV-QLQGSRVVVGAPQEIVAAN 58                                       </mat></sig></sig>

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112	2 TCSENTYVKGLCFLFGSNLKQQPQKFPEALRGCFQEDSDIAFLIDGSGSIIPHDFRRMKE 171 1	н
172	FVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGI	14
148	8 147	L -4
232	2 RKVVRELFNITNGAR-KNAFKILVVITDGEKFGDPLGYEDVIPFADREGVIRYVIGVGDA 290	000#
291	1 FRSEKSROELNTIASKPPRDHVPQVNNFBALKTIQNQLREKKFAIEGTQTGSSSSFEHEM 350	U 4, 4, 4,
351	1 SQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINWTRVDSDMNDAYLGYA 407       :         :         :	M M M M
408	8AAIILRNRVQSLVLGAPRXQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASL 461 	הביט <i>וכל פל</i> יו
462	2 CSVDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPLPRGQRARWQC-DAVLYGEQGPWGR 520	4.4.4.4
521	1 FGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR 580	A, O O III
581 433	1 LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLKSQPVLRVKAIMEFNPREVARNVFE 638	
639	9 CNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVEN 693	<b>о</b> п
694 545	4 ETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGN 748	С П
749	9 LRPVLAEDAQR-LFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGFREF 801	<b>о</b> п
802	2 NVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALK 861	0 1
862	2 STSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLE 919	<b>о</b> п
920	0 IPVKYAVYMVYTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFL 973	<b>о</b> п
974	4 VPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAV 1027	<b>У</b> П
1028	8 CQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFN 1076	<b>о</b> п
1077		J
916	6 GKEASVHIQLEGRPS-ILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVLLEGLH 974	ы

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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 158409; A49459
Oncogene 9, 611-619, 1994
A;Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small
A;Reference number: 158409; MUID:94119603; PMID:8290272
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cacule type: mRNA
A;Residues: 1-1035 & RES>
A;Crearences: UNIPROT:Q13797; GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g533327
A;Crearences: W.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A;Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partner A;Reference number: A49459; MUID:94064789; PMID:8245132
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Local Similarity 26.5%; Pred. No. 1.1e-34;
les 237; Conservative 160; Mismatches 332; Indels 164; Gaps
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Superfamily: integrin alpha-4 chain; Keywords: glycoprotein; metal binding; transmembrane protein; 1-27/Domain: signal sequence #status predicted <51G>
                                                                                                                                                          ntegrin alpha-9 chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-1035 <PAL>
A;Cross-references: GB:L24158
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0y 854 TEVGGALKSTSCSINRPIPPENSEVTRITEPUDGKASLGAKLALKANATSENNMERPHYR 913  Db 702 DFL	Db 344 SNRLSLSSTLIGGQIRSFEGLSIASIGDSNQDGFNDVAIGAPYEGDSAGAVYYHG-SAN 402  Qy 563 GISPSHSQRLS-PRLQYFQQSLSGQQDLTMDGLVDATVGAQGHVLLRSQPVL 619

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

January 13, 2005, 15:04:07; Search time 241.379 Seconds (without alignments) 2748.409 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

RWHUIB-A 5953 1 MALRVILLTALTLCHGFNLD.....FKRQYKDMMSEGGPPGAEPQ 1153

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P11215 homo sapien		Q9ji30 rattus norv	Q28984 sus scrofa	P20702 homo sapien		Q6kas4 mus musculu	Bad21383 mus muscu		Q9qye7 rattus norv		P20701 homo sapien	Oftyb8 bos taurus	15 bo	P24063 mus musculu	Q9wtv4 mus musculu			Q98tf0 cyprinus ca		Q8hzv0 bos taurus	O88340 rattus norv	Q60677 mus musculu	P38570 homo sapien	088341 rattus norv	homo	Q9ukx5 homo sapien	P53710 bos taurus	Q6p1c7 mus musculu	m	Q62469 mus musculu
SUMMARIES	ΙD	ITAM HUMAN	ITAM_MOUSE	Q9JI30	Q28984	ITAX_HUMAN	ITAD_HUMAN	Q6KAS4	BAD21383	ITAX_MOUSE	ITAD_RAT	ITAL_BOVIN	ITAL_HUMAN	Q6TYB8	AAQ90015	ITAL_MOUSE	Q9WTV4	Q9R200	Q98TF1	Q98TF0	096нв1	O8HZV0	088340	ITAE_MOUSE	ITAE_HUMAN	088341	ITA1 HUMAN	ITAH HUMAN	ITA2_BOVIN	Q6P1C7	AAH65139	ITA2_MOUSE
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## ALIGNMENTS

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Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)
                   SEQUENCE OF 17-31.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00342; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1A8X; Model; @=17-152.

PDB; 1BHO; X-ray; 1/2=-.

PDB; 1BHO; X-ray; 1/2=-.

PDB; 11DD; X-ray; 1/2=-.

PDB; 11DD; X-ray; @=140-331.

PDB; 11DD; X-ray; @=140-331.

PDB; 11MU; X-ray; @=140-331.

PDB; 1MU; X-ray; @=143-334.

PDB; 1MU; X-ray; A=144-337.

PDB; 1MSZ; X-ray; A=144-337.

PDB; 1MSZ; X-ray; A=144-345.

Genew; HGNC:6149; TGAM.

MIM; 120980; --.

GO; GO:000830; C:integrin complex; TA8.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR000413; Integrin_alpha.

PFam; PF01839; PG-GAP; 3.

PFam; PF00527; Integrin_alpha; 1.

PFam; PF00527; VWF, M.
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SMART; SM00327; VWA; 1.
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EMBL; M18044; AAA59491.1; -.
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PRINTS; PR00453; VWFADOMAIN.
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MEDLINE=98226734; PubMed=9560195;

A DOVAIG C., Springer T.A.;

Experimental support for a beta-propeller domain in integrin alpha-
ovavig C., Springer T.A.;

Experimental support for a beta-propeller domain in integrin alpha-
next and a calcium binding site on its lower surface.";

Froc. Natl. Acad. Sci. Us.A. 95.4870-4875(1998)

Proc. Natl. Acad. Sci. Us.A. 95.4870-4875(1998)

T. FUNCTION: Integrin alpha-W/beta-2 is implicated in various as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iG3b fragment of the third complement component. It probably recognizes the R-G-D C peptide in C3b. Integrin alpha-W/beta-2 is also a receptor for fibrinogen gamma chain.

C -1- SUBJUNT: Heterodimer of an alpha and a beta subunit. Alpha-M
                                                                                                                                                                                                                                                                                                        MEDLINE-87076671; PubMed=3539202; Pierre M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
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MEDLINE-95171458; PubMed=7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin (CR3 (CD11b/CD18).";
Cell 80:631-638(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDIJNE=5635671; PubMed=8747460;
MEDIJNE=5635671; PubMed=8747460;
"To, Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.

MEDLINE-98362595; PubMed-9687375;

Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,

Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,

Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,

Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;

"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                   SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318, PubMed=1683702;
Shollay C.S., Armout M.A.
"The promoter of the CDlib gene directs myeloid-specific and
                                                                                                                                                                                TISSUE=Blood;
MEDLINE=22144986; PubMed=1346576;
MEDLINE=22144986; PubMed=1346576;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                           developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure 3:1333-1340(1995)
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Db 960 LGQRSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1019  Qy 1021 VNCSIAVCORIQCDIPFFGIQEERATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF 1080	M MOUSE STANDARD; POSSES, QCRA73; POSSES, QCRA73; 01-NOV-1988 (Rel. 09, Creat 01-PEB-1991 (Rel. 17, Last 05-JUL-2004 (Rel. 44, Last	Integrin alpha-m pr subunit) (CR-3 alph Name=Itgam; Mus musculus (Mouse Eukaryota; Metazoa; Mammalia; Eutheria; NCBI TaxID=10090;		RP SEQUENCE FROM N.A. (ISOFORM 2).  RC STRAIN-CSTBL/6J; TISSUE-Spinal cord;  RX MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;  RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T.,  RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,	RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gasterland Tagriboldi M., Godzik A., Goudik J., Gratiboldi M., Grasis C., Godzik A., Goudi J., RA Grimond S., Gustinoich S., Hirokawa N., Jackson I.J., Jarvis B.D., RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,	RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M., RA Ravasi T., Reed J.C., Reed G.Z., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yang L., Yang Y., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., RA Hara A., Hashizume W., Imctani K., Ishini Y., Itoh M., Kagawa I., RA Hara A., Sakai K., Sakaki D., Shibata K., Shinagawa A., RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., RA Birney B., Hayashizaki Y., RA Birney E., Hayashizaki Y., RT "Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-length cDNAs.",	RN [3] RP SEQUENCE OF 11-45 FROM N.A. RC STRAIN=BALB/c; TISSUE=Spleen;
Table   1   16	QY         121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQL 180           Db         121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQL 180           QY         181 KKSKTLPSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPTTQLLGRTHTATGIRKVVRELFN 240           Db         181 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPTTQLLGRTHTATGIRKVVRELFN 240	241 ITNGARKUAFKILVVITDGEKFGDPLGYBDVIBEADREGVIRVVIGVGDAFRSEKSRQEL 300	QY         361 SNGPLISTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDWNDAYLGYAAAIILRNRVQSLV 420           Db         361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDWNDAYLGYAAAIILRNRVQSLV 420           QY         421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480           Db         421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480	HYYEOTRGGOVSVCPLPRGQRARWQCDAVLYGEGGQPHGRFGAALTVLGDVNGDKLTDVA HYYEQTRGGOVSVCPLPRGQRARWQCDAVLYGEGGQPHGRFGAALTVLGDVNGDKLTDVA HYYEQTRGGQVSVCPLPRG-RARWQCDAVLYGEGGQQPHGRFGAALTVLGDVNGDKLTDVA IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQGSLGGGQDLTWDGLV IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQGSLSGGQDLTWDGLV IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQGSLSGGQDLTWDGLV		Qy         721 NCIEDPVSPIVLRINFSLVGTPLSAFGNLREVLAEDAQRLFTALFPFEKNCGNDNICQDD 780           Db         720 NCIEDPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD 779           Cy         781 LSITFSFWSLDCLVVGGPREFVYTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS 840           Db         780 LSITFSFWSLDCLVVGGPREFVVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS 839	Qy         841 QRSWRLACESASTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA 900           Db         840 QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA 899           Qy         901 NVTSENNMPRTNKTEFQLELPVKXAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960           Db         900 NVTSENNMPRTNKTEFQLELPVKXAVYMVVTSHGVSTKXLNFTASENTSRVMQHQYQVSN 959	961 LGQRSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPV 1020

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GSLYQCDYSTGSCEPIRLQVPVEAVMMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120
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  PROSITE; PS50234; VWPA; 1.
Alternative splicing; Calcium; Cell adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
Signal; Transmembrane.
SIGNAL 1 16
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Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-1- SIMILARITY: Belongs to the integrin alpha chain family.
-1- SIMILARITY: Contains 7 FG-GAP repeats.
-1- SIMILARITY: Contains 1 VWFA domain.
                 Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note=No experimental confirmation available; IISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
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EMBL; AK03444; BAC30350.1; -.

EMBL; AK03444; BAC30350.1; -.

EMBL; ML499; AAA39484.1; -.

EMBL; ML499; AAA39484.1; -.

EMBL; ML499; AAA39484.1; -.

HSSP; P11215; IBHQ.

MGD; MGC: 96607; IEgam.

GO; GO:0008997; C:external side of plasma membrane; IDA.

GO; GO:000897; C:external side of plasma membrane; IDA.

GO; GO:000155; P:cell adhesion; IMP.

GO; GO:0030593; P:neutrophil chemotaxis; IMP.

InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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IsoId=P05555-1; Sequence=Displayed;
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MEDLINE=86287312; PubMed=2942940;
                                                                                                                                                                   SEQUENCE OF 17-28.
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              SEQUENCE FROM N.A.

Fathallah D.M. Sr., Zerria K. Jr.;

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-1- SIMILARITY: Belongs to the integrin alpha chain family.

HSSP: P11215; 1BHQ.

GO, GO:0001160; P:cell-marrix adhesion: IEA.

GO, GO:0007229; P:integrin-mediated signaling pathway; IEA.

InterPro; IPR000413; Integrin-alpha.

InterPro; IPR002035; VWF.A.
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Pfam; PF01839; PG-GAP, 2.
Pfam; PF01839; PG-GAP, 2.
Pfam; PF00185; Integrin_alpha; 1.
PRINTS; PR01985; INTEGRINA.
PRINTS; PR01985; INTEGRINA.
SWART; SW00191; Int_alpha; 5.
SWART; SW00327; VWA, 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0234; VWPA, 1.
PROSITE; PS05034; VWPA, 1.
PROSITE; PS05034; VWPA, 1.
PROSITE; PS05034; VWPA, 1.
PROSITE; PS05034; VWPA, 1.
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Best Local Similarity 73.4%; Pred. No. 1.8e-284;
Matches 846; Conservative 145; Mismatches 160; Indels
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                                                                                                  IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
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                       SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 26, Last annotation update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
10-MAR-2004 (TremBlrel. 26, Last annotation update)
10-MAR-2004 (Rat).
10-MAR-2004 (Mordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.NCBI_TAXID=10116;
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                                                                                             EBFRIHFTFKEFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKIL
                                                                                                                                          VVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVF
                                                                                                                                                       VVITDGEKFGDPLGYEDVIPEADRKGVIRYVIGVGDAFNSWKSREELNTIASKPCGDHVF
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  Length
 64.3%; Score 3826.5; DB 2; Length
79.8%; Pred. No. 4.1e-243;
ive 78; Mismatches 107; Indels
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                                                                                         STRDRLREGOIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP
              959 LGQRSFPVSVVFWIPVQINKVTIWDPPQVTFSQNLSSVCRTEQKSPSHSKFQDELERTPV
                                                                                                                                                                                                                                                                                          Let J. Schook L.B., Rutherford M.S.;

Let J.-K., Schook L.B., Rutherford M.S.;

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUIARI LOCATION: Type I membrane protein (By similarity).

-!- SIMILARITY: Belongs to the integrin alpha chain family.

EMBL; U40072; AAB16869.1; -- let integrin alpha chain family.

R GO; 600:0003160; P:cell-matrix adhesion; IEA.

R GO; 600:0003160; P:cell-matrix adhesion; IEA.

InterPro; IPR00203; VWFA.

R Pfam; PF01839; RG-GAP; 3.

R PRINTS; PR00453; VWFADOMAIN.

R PRINTS; PR00453; VWFADOMAIN.

R PRINTS; PR00453; VWFADOMAIN.

R SMART; SM00191; Int_alpha; 4.

R SMART; SM00191; Int_alpha; 4.

R SMART; SM0027; VWA; 1.

R PROSITE; PS50234; VWFA.

T NON_TER 920 920

O SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;
                                             NCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD
                                                                                                                                                                                                                                 LGORSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                                                                                                                                                                                                                             VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Sus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae,
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Q28984;
01-NOV-1996 (TEMBLrel. 01,
01-FEB-1997 (TEMBLrel. 02,
01-JUN-2003 (TEMBLrel. 24,
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MMNEAGGODGPPQ 1151
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SEQUENCE FROM N.A.
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 199
                                             721
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DATABASE: NAME=PROW; NOTE=CD guide CD11c entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
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Potential
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N-linked
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EMBL; M29165; -; NOT ANNOTATED CDS.
EMBL; M29482; AAA51620.1; ALT SEQ.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29486; AAA51620.1; JOINED.
EMBL; M29586; AAA51620.1; JOINED.
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FG-GAP
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     MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.N.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.N.,
A Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Sheverchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.,
Sadeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87167596; PubMed=3549901;
W MEDLINE-87167596; PubMed=3549901;
MILLEr L.1., Wiebbe M., Springer T.A.;
MILLEr L.1., Wiebbe M., Springer T.A.;
MILLEr L.1., Wiebbe M., Springer T.A.;
T and p150,95 leukocyte adhesion proteins.";
U. Immunol. 138:12381-2383 (1987).
C - FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-PR in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially improvated in monocyte adhesion and chemotaxis.
C --- SUBCNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.
C --- SUBCELMUAR LOCATION: Type I membrane protein.
C --- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytes.

DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=8816665; PubMed=3327687; Corbi A.L., MILLE-LJ., O'Connor K., Larson R.S., Springer T.A.; Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; CDMA cloning and complete primary structure of the alpha subunit of leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
01-FEB-1991 (Rel. 17, Created)
05-701-2004 (Rel. 44, Last sequence update)
01-071-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu MS).
Name=ITGAX; Synonyme=CD11C;
Homo sapiens (Human).
                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 265:2782-2788(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.eib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
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(Potential).
(Potential).
(Potential).
(Potential).
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Extracellular (Potential).
Potential.
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FG-GAP 1.
FG-GAP 2.
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MIM; 151510; -
GO: 000010305; C: integrin complex; TAS.
GO: GO: 00004872; F: receptor activity; TAS.
GO: GO: 0000155; P: receptor activity; TAS.
GO: GO: 0000155; P: receptor activity; TAS.
GO: GO: 00001887; P: receptor activity; TAS.
InterPro: IPR000413; Integrin_alpha.
InterPro: IPR000413; Integrin_alpha.
PFam; PF001839; FG-GAP; 3.
PFam; PF00092; VWA; 1.
PRINTS; PR00092; VWA; 1.
PRINTS; PR00191; Int alpha; S.
SWART; SM00191; Int alpha; S.
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCN
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604
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                        RYQHIGKAVIFTQVSRQWRMKAEVTGIGSYFGASLCSVDVDTDGSTDLVLIGAPHYYE
                                                               RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
                                                                                            GEEDNRGAVYLPHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
                                                                                                       GAQCHVILLIRSOPVILRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD
                                                                                                                                               345 HLTCDSAPVG--SQCTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS
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                                                                                                                                                                            RLREGOIOSVVTYDLALDSGRPHSRAVFNETKNSTRROTOVLGLTOTCETLKLOLPNCIE
                                                                                                                                                                                                                    DPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT
                                                                                                                                                                                                                                                           FSPMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW
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Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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AC 013349; Q15575; Q15576; Q15776; Q1 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 44, Last annotation update)

DT 05-UUL-2004 (Rel. 44, Last annotation update)

DE Integrin alpha-D precursor (Leukointegrin alpha DR Name-ITGAD; GN Name-ITGAD; GN HOMO sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
FISSUE-Spleen;
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                           T -> S (in Ref. 4).
T -> A (in Ref. 4).
T -> S (in Ref. 4).
G -> A (in Ref. 4).
E -> K (in Ref. 4).
D -> L (in Ref. 1).
I -> V (in Ref. 1).
SEK -> TPHYPQDNV (in Ref. 4).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE=96257236; PubMed=8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; Cloning and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit.";
                                                                                                                                                                                                                                                                                     MEDLINE=99059812; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                       Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin
gene CD114. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99370002; PubMed=10438935; Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Graygon M.H., Bochner B.S., Gallatin W.M., Staunton D.E.; The leukcoyte integrin alpha D beta 2 binds VCMM-1: evidence for a binding interface between I domain and VCAM-1."; Jumunol. 163:19944-1990(1999).
J. Immunol. 163:19944-1990(1999).
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GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0016337; P:cell-cell adhesion; NAS.
                                                            SEQUENCE OF 1-235 FROM N.A.
MEDLINE=20187620; PubMed=10722744;
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U40277; AAB60637.1; -.
U40279; AAB60638.1; -.
U40278; AAB60638.1; JOINED
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U40274; AAB60634.1; -.
U40275; AAB60635.1; -.
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HSSP; P11215; 1BHQ.
Genew; HGNC:6146; ITGAD.
                               Immunity 3:683-690(1995)
                                                                                                                                                                                                                                             Gene 171:291-294 (1996).
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INTERACTION WITH VCAMI
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125 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
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R GO; GO:0007160; P:cell-matrix adhesion; NAS.
R InterPro; IPR000413; Integrin_alpha.
R InterPro; IPR000413; Integrin_alpha.
R InterPro; IPR000413; Integrin_alpha.
R Pfam; PF00183; FG-GAP; 3.
R Pfam; PF00185; Integrin_alpha; 1.
R PRIMTS; PR00185; INTEGRINA.
R PRIMTS; PR00185; INTEGRINA.
R PRIMTS; PR00185; INTEGRINA.
R SWART; SW00191; Int alpha; 5.
R SWART; SW00191; Int alpha; 5.
R PROSITE; PS00242; INTEGRIN ALPHA; 1.
R PROSITE; PS00242; INTEGRIN ALPHA; 1.
R PROSITE; PS0034; VWFA; 1.
R R PROSITE; PS0034; VWFA; 1.
R R R PROSITE; PS0034; VWFA; 1.
R R PROSITE; PS0034; VWFA; 1.
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R R PROSITE; PS0034; VWFA; 1.
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A Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; The Cading of the Coding Sequences of Mouse Homologous of Fild Genes: The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs Identified by Screening of Terminal Sequences of CDNA Clones Randomly Sampled from Size-Fractionated Libraries."; DNA Res. 11:167-180(2004) Type I membrane protein (By similarity).

-: SUMILARITY: Belongs to the integrin alpha chain family.

-: SIMILARITY: Belongs to the integrin alpha chain family.

REBL; AKISII33; BAD21381.1; -.

REBL; AKISII33; BAD21381.1; -.

RICHEPRO; IPRO00413; Integrin_alpha.

RICHEPRO; IPRO00413; Integrin_alpha.

REPAM; PF00957; Integrin_alpha; 1.

Pfam; PF00957; Integrin_alpha; 1.
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Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Eutheria; Rodentia;
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           Name=mFLJ00114;
Mus musculus (Mouse)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Length 1188;

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Query Match

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                                            LLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQ
                      Gaps
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57.2%;
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"Isolation of genes selectively expressed by dendritic cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
I submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Interaction alpha ar/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis (By similarity).

-!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2 (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-!- DOMAIN: The integrin 1-domain (insert) is a VWFA domain. Integrins with 1-domains do not undergo protease cleavage.

-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its moch non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
1041 HMQKSPVLDCSIADCLHLRCDIPSLGILDELYFILKGNLSFGWISQTLQKKVLLLSEAEI 1100
                                       1074 LENDSVFTLLPGQGAFVRSQTETKVBPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGF
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PROSITE; PS50234; VWPA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
Name=Itgax;
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.
Tsuchiya H.;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:9660; Itgax.
GO; 0000899; Itgax.
GO; 0000899; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
PRINTS; PR0145; INTEGRINA.
PRINTS; PR0145; INTEGRINA.
SMART; SM00191; Int alpha; 5.
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Integrin alpha-X.
Extracellular (Potential).
                                                                                                                                                                        PRT; 1169 AA
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SIGNAL 1 19 E
CHAIN 20 1169 E
DOMAIN 20 1116 E
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                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                      (Potential). (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                                                                                                       (Potential)
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Cytoplasmic (Potential). FG-GAP 1.
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FG-GAP 4.
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1161 AA;
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SEQUENCE FROM N.A.

O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,

O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,

Gallatin W.M., VanderVieren M., Kilgannon P.D., Dietsch G.,

Gallatin W.M., VanderVieren M., Kilgannon P.D., Dietsch G.,

AT "Cloning of rat alpha D, a novel beta 2 integrin.";

Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

L. FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and

VCAM1. May play a role in the atherosclerotic process such as

Clearing lipoproteins from plaques and in phagocytosis of blood-

borne pathogons, particulate matter, and senescent erythrocytes

C clearing lipoproteins from plaques and in phagocytosis of blood-

borne pathogons, particulate matter, and senescent erythrocytes

C from the blood (By similarity).

C -1- SUBGNAT: Heterodimer of an alpha and a beta subunit. Alpha-D

associates with beta-2 (By similarity).

C -1- SUBGNATN: Type I membrane protein (By similarity).

C -1- DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins

With I-domains do not undergo protease cleavage.

-1- SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                954 HOYOVSNIGORSLPISLVFLVPVRLNOTVIWDRPOVTFSENLSSTCHTKERLPSHSDFLA 1013
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        SFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQ------
                                                                                                                                                                                                                                                PVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITF
                                                                                                             GPPDLKTLVVGSDLELNVDVTVSNDGEDSYGTTVTLFYPVGLSFRRVAEGQVFLRKKEDQ
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                                                    LREGOIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIED
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAD RAT STANDARD; PRT; 1161 AA. 090XE7; 05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 05-JUL-2004 (Rel. 44, Last annotation update)
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Name=Itgad;
Rattus norvegicus (Rat).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002035; VWF.A.
Fram, PF01039; FG-GAP; 3.
Pfam; PF00092; VWA; 1.
PFam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00191; Int. alpha; 5.
SWART; SM00191; Int. alpha; 5.
SWART; SM00191; VNFADOWAIN.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50244; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
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FG-GAP 2.
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FG-GAP 5
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HSSP; P11215; 1BHQ.
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                                                                   SKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNIT
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SENNKPDTNKTAFQLELPVKYTVYTLISRQEDSTNHVNFSSSHGGRRQEAARYRVNNL
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Gene 325:97-101 (2004).

Gene 325:97-101 (2004).

Gene 325:97-101 (2004).

I. FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAMZ, ICAMI and ICAMI and ICAMI are involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes (By similarity).

-!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L associates with beta-2 (By similarity).

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY267467; AAP94035.1; -.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50244; VWFA; 1.
Calcium; Cell_adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;
Fett T., Zecchinon L., Baise B., Desmecht D.;
"The bovine (Bos taurus) CDIa-encoding cDNA: molecular cloning,
characterisation and comparison with the human and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin alpha-L.
Extracellular (Potential)
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
Potential.
GFFKR motif.
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FG-GAP 2.
VWFA.
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ITAL BOVIN STANDAF
P61625;
05-JUL-2004 (Rel. 44,
05-JUL-2004 (Rel. 44,
                                                                                                                             Bos taurus (Bovine).
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                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                   (CD11a).
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Name=ITGAL;
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POVTFS-ENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFN 1045
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P20701; 043746;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
11tegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
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                                                                                                                                                                                                                                                         TKYLNFTASENTSRVMQHQYQV----SNLGQRSLPISLVFLVPVRLNQTVI----WD---R
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MEDIINE=89139587; PubMed=2537322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
"Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
       QGLSFRKVBIL---KPHSHVPVGCBELPBEAVVHS-RALSCNVSSPIFGEDSMVDIQVMF
                                                                                                                                                               DVDSKASLGNKLLLKANVTS-----ENNMPRTNKTBFQLELPVKYAVYMVVTSHGVS
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                                                                        LDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITF
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"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha
beta 2) integrin.";
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MEDLINE-99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon I Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Beslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell & Eichler E.B., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA schuman chromosome 16p and 16q.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF 153-335, AND
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Catarrhini; Hominidae;
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MEDLINE=96398682; PubMed=8805579;
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MEDLINE=96036067; PubMed=7479767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily.";
J. Cell Biol. 108:703-712(1989)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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t; Pred. No. 4.8e-95;
200; Mismatches 475; Indels 108;
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                   the CD11a/CD18 integrin.";

LE Structure 4:931-942(1996).

N [5]

X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.

X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.

X Rallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G., Cottens S., Weitz-Schmidt G., Hommel U.;

Cottens S., Weitz-Schmidt G., Hommel U.;

Tructural basis for LFA-1 inhibition upon lovastatin binding to the "Structural basis for LFA-1 inhibition upon lovastatin binding to the "Structural basis for LFA-1 inhibition upon lovastatin binding to the "Structural basis for LFA-1 inhibition upon lovastatin binding to the "I b Mol. Biol. 29:1-9(1999).

LI Mol. Biol. 29:1-5(1999).

LI FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoid=20701-2; Sequence=VSP 002738;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Leukocytes.
-!- DOMAIN: The integrin 1-domain (insert) is a VWFA domain. Integrins with 1-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd1la.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRESIDENT STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND S
                                                                                                                                                                                                                                                                                                                                    and monocytes.
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
                                                                                                                                                                                                                                                                                                                                                                               associates with beta-2.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=P20701-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC002310; AAC31672.1; -. S03308; S03308.
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N-linked (GlCNAc. ..) (Potential).
Q -> QGVHGLVEMQTSKQILCRPAGDAEHTVGAQEGELPC
PWGVSEAFRDIRACECR (in isoform 2).
                                                                                                                                                                                                                                            (Potential).
(Potential).
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(Potential).
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                                                                                                                                                                                                                                                                                                                             (Potential
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Pred. No. 1.6e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128819 MW; 39A7AF92EF286FC0 CRC64;
Integrin alpha-L.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                      R -> W (in Ref. 1 and 2).
Y -> I (in Ref. 2).
                    Potential.
Cytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
                                                                                                                                                                                                                                                                                                                                       (GlcNAc. .)
                                                                                                                                                  GFFRR motif.
By similarity.
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                                                                     FG-GAP 4
FG-GAP 4
FG-GAP 5
                                                                                                    FG-GAP
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Best Local Similarity ' 34.3%;
                                                                                                                        323 37
1170 AA;
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Mon Feb

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IQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVE 1099
                           63 GNSMGNLYQCQPETGDCLPVTLS--SNYTSKYLGWTLATDPTSDNLLACDPGLSRTCDQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 ANORGSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                       1083 VVYEKQMLYLYVLSGIGGLLILLIFIVLYKVGFFKRNLKEKMEAGRGVPNGIP 1136
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                         PFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEG-GPPGAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 108;
                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7B8D8AFBA896C9DF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.2%; Score 1557; DB 2; 34.2%; Pred. No. 2.5e-93;
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PROSITE; PS50234; VWF9; 1.
Call adhesion; Integrin; Transmembrane
SEQUENCE 1166 AA; 128723 WW; 7B8DB.
                                                                                                                                                             (TrEMBLrel. 27, Created)
                                                                                                                                         PRT;
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
                                                                                                                                        PRELIMINARY;
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411; Conserv
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                                                                   114
                                                                                --GNSTGSLYQCQSGTGHCLPVTLR-GSNYTSKYLGMTLATDPTDGSIIACDPGLSRTCD 120
                                                                                                               ENTYVKGLCFLFGSNLR----QQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMK 170
                                                                                                                               EFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATG 230
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                        54
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                                                                  55 VAANQRGSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCS
                                                                                                                                                                          FPENSEVTFNI TFDVDSKASLGNKLLLKANVTSENN----MPRTNKTEFQLELPVKYAVY
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                      ----NLDTENAMTRQ--ENARGEGOSVVQLQGSRVVVGAPQEI
 Gaps
464; Indels 110;
Mismatches
211;
Conservative
                      6 LLLTALTLCHGF
409;
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Matches 411
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                                                                                                                                      1086 MLYLYVLSGIGGLILLFLIFILIYKVGFFKRILKEKMEANVDASSEIPGEDAGQPELEKE 1145
                                  PQVTFS-ENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFN 1045
                                                                              1046 ATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPN 1105
                                                                                                                         1106 PLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM------SEGGPPGAEPQ 1153
                                                       PPVNCSPRNLESPSDEAE----ROEIL 1027
TLYISFIPKSPRIHHVKHIYQVRIQPSNYDNMP-PLBALVRVPRVHSBGLITHKMSIQME 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leukocytes recruitment.
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Leukocytes.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Contains 7 FG-3Ap repeats.
SIMILARITY: Contains 7 FG-3Ap repeats.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                           1028 VQVNGMVELRGTIKAS-SMLSLCSSLAISFNSSKHFHLHGRNASM-AQVVMKVDLVYEKE
                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91268576; PubMed=2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
alpha-subunit and its expression in COS cells.";
J. Immunol. 147:369-374(1991).
                                                                                                                                                                                                      PRT; 1163 AA
                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85188276; PubMed=3887182;
                                                                                                                                                                                                                              (Rel. 21, Created)
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PIR; I56126; I56126.
                                                                                                                                                                                                                                                                                                Name=Itgal; Synonyms=Lfa-1;
                                                                                                                                                                                                      STANDARD;
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HSSP; P20701; 1DGQ.
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                                                                                                                                                                                                                                                                                     (CD11a).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                 PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
SIGNAL
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(Potential).
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Extracellular (Potential)
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LCNAC.
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FG-GAP 4.
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR0002035; VWF A.
Pfan; PF01839; FG-GAP; 2.
Pfan; PF001837; Integrin_alpha; 1.
Pfan; PF00092; VWA; 1.
PRINTS; PR001185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int alpha; 5.
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FG-GAP 2
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:    :  :  :             : :          : :	232 RKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYV 284	285 IGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKKFAIEGTQTGSSS 344   :    :     ::  :  :     :        :	345 SFEHEMSQEGFSAAITSNGFLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDWNDAY 403	404 LGYAAA-IILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGAS 460      -  -  -  -  -  -  -  -  -  -  -  -	461 LCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGR 520 	521 FGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR 580 	581 LQYFGOSLSGGQDLTWDGLVDLTVGAQGHVLLLIRSQPVLRVKAIMEFNPREVARNVFECN 640 :::  :  :	641 DQVVKGKEAG-EVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNST 699 :::	700 RRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGN-LRPVLAE 755   : :	756 DAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRN 809 753 SIHTV-TKEIPFEKNCGEDKKCEANLTLSSPARSGPLRLMSSASLAVEWILSN 804	810 DGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGAL-KSTSCSIN 868	869 HPIFPENSEVTFNITFDVDSKASLGNKLALKANVTSEN-NMPRTNKTEFQLELPVKYAVY 927 	928 MYVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPLVPRLNQTVIMDRP 987 ::	988 QVTFSENLSSTCHTKE-RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFF 1038	GIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKV		
: 176 MKI												869 HPI	928 MVV :: 920 ILT	988 Q		1099 EPF	1078 DLI
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Search completed: January 13, 2005, 15:18:42 Job time : 249.379 secs

5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2005

- protein search, using sw model OM protein

January 13, 2005, 14:59:41 ; Search time 215.571 Seconds (without alignments) 1918.696 Million cell updates/sec Run on:

1 MALRVLLLTALTLCHGFNLD.....FKRQYKDMMSEGGPPGAEPQ 1153 RWHU1B-A Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62DX Scoring table:

2002273 Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2001s:\* geneseqp2002s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw65090 Human Bet	Aab07360 Human CD1		Abg61469 Human Bet		Add25615 Binding d	Aar04136 Alpha sub	Adm99589 Human int	Adp12435 Protein e	Adp44061 Human CD1	Adno2004 Human inf	Adg17510 Human sof	Aar07120 p150.95 a	Aaw65091 Human Bet	Aab07361 Human CD1	Abg61470 Human Bet	Abu07406 Protein d	Adg32005 Human hom	Aar78166 Human bet	Aaw23049 Human bet	Aaw57491 Human bet	Aaw65089 Human Bet	Aaw72825 Human alp	Aaw73342 Human alp	Aab07359 Human alp
ID	AAW65090	AAB07360	AAU80252	ABG61469	AA014428	ADD25615	AAR04136	ADM99589	ADP12435	ADP44061	ADN02004	ADQ17510	AAR07120	AAW65091	AAB07361	ABG61470	ABU07406	ADG32005	AAR78166	AAW23049	AAW57491	AAW65089	AAW72825	AAW73342	AAB07359
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\$ Query Match	100.0	100.0	100.0	100.0	100.0	100.0	8.66	7.66	99.6	59.0	58.8	58.8	58.6	58.4	58.4	58.4	58.4	58.4	58.0	58.0	58.0	58.0	58.0	58.0	58.0
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<b></b>	Aaw60004 Rat alpha Aaw72824 Rat alpha Aab07374 Rat alpha
ABG61468 AAW23064 AAW5106 AAW72837 AAW73343 AAW72837 AABG7376 AG61485 AAW52061 AAW72836 AAW72836 AAW73836 AAW73847 AABG7482 AAW73847 AABG7482 AAW73847 AAW7886	AAW60004 AAW72824 AAB07374
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## ALIGNMENTS

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis. Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA (first entry) 28-SEP-1998 AAW65090; RESULT 1 AAW65090 

Homo sapiens US5728533-A. 17-MAR-1998

94US-00286889. 94US-00362652. 93US-00173497. 95US-00485618 07-JUN-1995; 05-AUG-1994; 21-DEC-1994; 23-DEC-1993;

Van Der Vieren M, Gallatin WM;

(ICOS-) ICOS CORP.

WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comparising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

rwhulb-a.rag

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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukcyte have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha approximately 60% identity to the protein sequence of alpha_d. The approximately 60% identity to the protein sequence of alpha_d. The Alpha_d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatold arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
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                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                           GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.
                                     961 LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKADV
                                                                                                                                                                                                                                                                                              TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKD
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This invention relates to a modified integrin-I or integrin I-like domai polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or imunosuppressive activities. The polypeptides of the invention have an open conformation and are useful a immunogens to produce antibodies that selectively bind to integrin I-domain, and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease,
                                                                                        1021 VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                                                               LGORSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                         VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                                                 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
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                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disease, autoimmune disorder; Crohn's disease;
human immunodeficiency virus; HIV; myocardial infarction;
Sjorgen's syndrome; rheumatoid arthritis.
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inhibition of macrophage infiltration at the site system injury. The monoclonal antibodies can also
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                                                                                                                1, Mismatches
                                                                                      Score 5953;
Pred. No. 0;
                                                                                                   Pred. No.
                                                                                     100.0%;
                                                                                                   dest Local Similarity 99.9
Attches 1152; Conservative
             system injury. The monocl
diagnose Crohn's disease
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Sjorgen's syndrome, rheumatoid arthritis, dermaitis. A therapeutic, composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antiqenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-1 alpha-M protein subunit used to generate the mutant polypeptides of the invention.
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 nephritis; human immunodeficiency virus (HIV),
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99.9%; E
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1140 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140 The invention relates to promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-I; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; locomotor recovery; locomotor damage; locomotor impairment; an anti-alpha-d monoclonal antibodies for promoting locomotor y, inhibiting locomotor damage, limiting locomotor impairment, or ig autonomic and sensory dysfunction following spinal cord injury. LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPV TLLPQQAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA LGQRSLP1SLVFLVPVRLNQTV1WDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV VNCSIAVCQRIQCDIPFFGIQEFFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF NVTSENNMPRTNKTEFQLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 3eta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD; autonomic dysfunction; sensory dysfunction; spinal cord injury Human Beta2 integrin alphaCD11b subunit. Example 5; Page 191-194; 270pp; English. Ä. ABG61469 standard; protein; 1153 Van Der Vieren L5-OCT-2001; 2001WO-US032059 13-OCT-2000; 2000US-00688307 MMSEGGPPGAEPQ 1153 MMSEGGPPGAEPO 1153 (first entry) WPI; 2002-463260/49. Gallatin WM, Homo sapiens (ICOS-) ICOS 27-AUG-2002 18-APR-2002. 1021 961 1021 1081 1141 901 1081 1141 ABG61469 limiting οŧ ABG61469 RESULT Ор 셤 õ g ò 셤 ò à ò 

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spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphab can implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alphab protein sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mac-1; integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related immunological desorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
                                                                                                                                             TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
               QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITPDVDSKASLGNKLLLKA
                                                                               NVTSENNMPRINKTEFQLELPVKYAVYAVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN
                                                                                                                            LGORSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                                                                                                                                           VNCSIAVCQRIQCDIPFFGIQEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                                                                                                                                                                         TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
ORSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
                                                            NVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN
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The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. theumatorid arthritus). The variant integrin I domain proteins and nucleic acids can also be used for treating: ischaemial reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for bloactive agents. The present amino acid sequence represents the Mac-1 alpha subunit of integrin
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1020 Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; fall constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent condition; B-call disorder; melannoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease. 900 The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease. QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA LGGRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV TLLPGGGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD NVTSENNMPRTINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV VNCSIAVCORIOCDIPFFGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF TLLPGQGAFVRSQTETKVEPFEVPNPLPL1VGSSVGGLLLLALITAALYKLGFFKRQYKD VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF Binding domain-immunoglobulin fusion protein-associated protein Thompson Disclosure; SEQ ID NO 176; 157pp; English Ą. Ledbetter JA, Hayden-Ledbetter MS, ADD25615 standard; protein; 1153 17-JAN-2001; 2001US-0367358P. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P. 25-JUL-2002; 2002US-00207655 1141 MMSEGGPPGAEPQ 1153 1141 MMSEGGPPGAEPQ 1153 (first entry) (GENE-) GENECRAFT INC WPI; 2003-801317/75. US2003118592-A1 Inidentified, 15-JAN-2004 26-JUN-2003 1081 901 961 196 1021 1021 1081 901 ADD25615; ADD25615 RESULT ò 셤 ò 셤 ò ద ò 셤 ò 셤

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hinge region polypeptide, a mutated human 1gG1 immunoglobulin hinge region polypeptide, a mutated human 1gG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide contains to contains to contains to contains to contains a cysteine residues, where the first cysteine is not mutated; a mutated human 1gG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human 1gG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues a mutated human 1gG1 immunoglobulin hinge region polypeptide contains no cysteine residues a mutated human 1gG1 immunoglobulin hinge region polypeptide contains on cysteine residues are an isolated polymulectide encoding the ninding domain-immunoglobulin fusion protein, a recombinant expression antigen. Also included are an isolated polymulectide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion construct, producing the binding domain-immunoglobulin fusion construct, producing the binding domain-immunoglobulin fusion construct, and treating a subject to subject having or suspected of having a malignant condition or a B-cell fusion protein or polymuclectide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. mallanged main-immunoglobulin fusion protein is useful formed and subject having or suspected of having a malignant condition or a B-cell consumed at a for this patent formed protein sequence is a binding domain-immunoglobulin himpulation fusion protein equenc
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Matches 1152, Conservative
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                                    IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
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/label= putative N-glycosylation site
240. .242
/label= putative N-glycosylation site
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/label= signal_peptide
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Best Local Similarity 99.8 Matches 1151; Conservative

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                                 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
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Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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                                                               1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
                                                                                                                              GSLYQCDYSTGSCEPIRLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, e.g. nectanical organ replacement rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
1080 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGILLLALITAALYKLGFFKRQYKD
                                                                                                                                                                                                                                                                                                                                                         transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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20-DEC-2002; 2002US-00325899.
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                                                                                                                MMSEGGPPGAEPO 1153
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                                                                                                    XXSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVXPITQLLGRTHTATGIRKVVRELFN
                                                                                                                                                                                        NTIASKPPRDHVFQVNNFBALKTIQNQLREKKFAIBGTQTGSSSSFEHEMSQEGFSAAIT
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        GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
                                                           GLCFLFGSNIRQOPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL
                                                                                                                                                     241 IINGARKNAFKILVVIIDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL
                                                                                     KKSKTLFSLMQYSEEFRIHFTFKEFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFN
                                                                                                                                      ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL
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Score 5930.5; Pred. No. 0; 1; Mismatches

99.6%; ilarity 99.7%; Conservative 1

Best Local Similarity Matches 1150; Conserv

Query Match

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Identifying an inhibitor of human immunodeficiency virus (HIV) entry into a human host cell useful for preventing and/or treating HIV infection, by identifying an inhibitor of a cell surface polypeptide such as CXCR-4.
                                                                                                                       HIV entry inhibitor; cell surface protein inhibitor; HIV infection; anti-HIV; virucide; HIV uptake inhibitor; human; CD11C; integrin alpha X.
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 14; 133pp; English.
                                                        ADP44061 standard; protein; 1163 AA
                                                                                                        Human CD11C protein SEQ ID NO:14
                                                                                                                                                                                                 08-DEC-2003; 2003WO-US039208
                                                                                                                                                                                                                  06-DEC-2002; 2002US-0431522P
1153
            1140 MMSEGGPPGAEPQ 1152
                                                                                        (first entry
MMSEGGPPGAEPQ
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N-PSDB; ADP44060.
                                                                                                                                                                                                                                 (PPDP-) PPD DEV LP
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                                                                                                                                                                 WO2004053094-A2
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                                                                                                                                                 Homo sapiens
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The present invention describes a method (M1) for identifying an inhibitor of HIV entry into a human host cell. (M1) comprises identifying an inhibitor of a cell surface polypeptide selected from CXCR-4 (352.2 anino acids, SEQ ID NO:8, ADP44052), CCR4 (350 amino acids, SEQ ID NO:19, ADP44052), CCR7 (378 amino acids, SEQ ID NO:12, ADP44053), CDR4 (350 amino acids, SEQ ID NO:16, ADP44063), CDR4 (354 amino acids, SEQ ID NO:18, ADP44065), CDR9 (199 amino acids, SEQ ID NO:20, ADP44063), CDR9 (354 amino acids, SEQ ID NO:20, ADP44063), CDR3 (365 amino acids, SEQ ID NO:20, ADP44063), CDR3 (365 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:30, ADP44077), CCC (462 amino acids, SEQ ID NO:32, ADP44077), ADP44081), PAXI (150 amino acids, SEQ ID NO:30, ADP44077), CCC (462 amino acids, SEQ ID NO:32, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:32, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (1009 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (1009 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (1009 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:32, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP44081), CR PKCS (576 amino acids, SEQ ID NO:30, ADP4
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Query Match 59.0%; Score 3514; DB 8; Best Local Similarity 61.4%; Pred. No. 1.4e-278; Matches 701; Conservative 139; Mismatches 295;
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1084 PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMMS 1143 RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023 1083 365 485 844 902 963 124 304 364 424 484 544 604 604 664 664 724 724 784 784 904 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKBFVSTVMEQLKKSK 184 67 426 RYQHTGKAVIFTQVSRQWRMKAEVTGTQIGSYFGASLCSVDVDSDGSTDLVLIGAPHYYE **QCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCP** TLPSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYB **QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP** GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD 665 LLGSRDLQSSVTLDLALDPGRLSPRATFQETKNRSLSRVRVLGLKAHCENFNLLLPSCVE DPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW FSPPGLKSLLVGSNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGOKOGLRSL 345 RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS ENNMPRINKTEFOLELPVKYAVYMVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ SIAVCORIOCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE 963 1 665 725 905 964 125 245 306 486 545 485 545 605 605

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RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023
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                                                QTRGGQVSVCPLPRGWR-RWWCDAVLYGEQGHPWGRFGAALIVLGDVNGDKLTDVVIGAP
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                                                                                                                                                                                                                                                                                                                          marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa;
FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; Mip-1(beta);
L-selectin; EGFL6; IDO; IL-8; CD11c; TLR2; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises marker genes for inflammatory bowel disease (IBI - FcgammaR IIIa, FcgammaR IIIb, Mig, NRG-2, hexokinase, HM74, REG III, LPAP, Mip-1(beta), L=selectin, EGFL6, IDO, IL-8, CD11c, and TLR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colitis and Crohn's disease). The present amino acid sequence represents an IBD marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic agent for IBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY
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                                                                                                                                                                                                                                                                                        Human inflammatory bowel disease marker - CD11c protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; SEQ ID NO 27; 151pp; Japanese.
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Matches 699; Conservative 139;
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                                                                                                                                                                                                                                                    (first entry)
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N-PSDB; ADN01990.
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the
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                                             soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human
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                                                                                                                                                                                                                                                                                                                         Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQFSLMQPSNKFQTHFTFEEFRTSNPLSLLASVHQLQGFTYTATAIQNVVHRLFHASYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification per se but was submitted in CD format by the inventor
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                 - SEQ ID 327
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                 protein
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 327; 210pp; English
                sarcoma-upregulated
                                                                                                                                                                                                                                                                  Zlotník A;
                                                                                                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC
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                tissue
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PGQGAFVRSQTETXVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
                                          QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP
                                                                                     GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD
                                                                                                                                                                                                                                            DPVSPIVLRLNFSLVGTPLSAFGNLRPVLABDAQRLFTALFPFEKNCGNDNICQDDLSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIAGCLRFRCDVPSFSVQEELDFTLKGNLSFGWVRQILQKKVSVVSVAEITFDTSVYSQL
                               RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
                                                                                                                GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
                                                                                                                                                                                                   RLREGOIOSVVTYDLALDSGRPHSRAVFNETKNSTRROTOVLGLTOTCETLKLOLPNCIE
                                                                                                                                                                                                                                                                                      FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW
                                                                                                                                                                                                                                                                                                                              RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS
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(first entry)
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58.6%; Score 3491; DB 2;
61.1%; Pred. No. 1.1e-276;
ive 139; Mismatches 299;
                              // Jabel= glycosylation site
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/label= clycosylation 8.
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1050. .1052
/label= glycosylation s
1108. .1133
/label= transmembrane
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|abel= signal peptide
               20. .44
/label= N-terminus
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N-PSDB; AAQ06068.
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Matches
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sub-a beta Clone lambda X47 was isolated from a cDNA library constructed from:total RNA extracted from phorbol myristate acetate stimulated HL-60 myelomonocytic cells. The library was screened with oligonuclectide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhindviral infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAQ06068, AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.) Treatment of viral esp, rhino-viral infection - by admin. of alpha unit of p150.95 cell surface adhesion receptor, opt. together with chain of CD-18 family. Disclosure, Fig 3, 59pp, English

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124
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                   5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY
                                QCDYSTGSCEPIRLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCF
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305 365 304 364 424 425 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184 484 485 544 544 604 604 664 724 724 784 784 904 963 GEBENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGCQDLTQDGLVDLAV ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA SKPPRDHVPQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP RYOHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP OTRGGOVSVCPLPRGWR-RWWCDAVLYGEOGHPWGRFGAALTVLGDVNGDKLTDVVIGAP GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD RLREGOI OSVVTYDLALDSGRPHSRAVFNETKNSTRROTQVLGLTQTCETLKLQLPNCIE DPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW FSFPGLKSLLVGSNLELNAEVMVMNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSL 845 HLTCDSA--PVASQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS PGQERFWRAQTTTVLEKYKVHNPTPLIVGSSIGALLLLALITAVLYKVGFFKRQYKEMME RLACESASSTEVSGALKSTSCSINHPI PPENSEVTFNI TFDVDSKASLGNKLLLKANVTS ENNMPRINKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC SIAVCORIQCDIPFFGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS E 1144 365 128 186 305 908 366 486 545 665 245 425 426 485 545 605 605 725 725 785 785 903 964 1024 1023 1084 1083 1144 905 963 셤 8 & ò 셤 à 셤 8 셤 ઠે ద ò ద දු පු 8 8 ò g 8 ద ò 유 상 유 요 ò g 셤 ⋧ à 셤 ⋩ 임 8 8

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RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023
                                 246 ARRDAIKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKELNDIA
                                                                                                                                                   DSVIPILERENFILVGKPELAPRNERPMLAALAQRYFTASLPFEKNCGADHICQDNLGIS
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                                                                                          RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
                                                                                                                                                                                                                                                       QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP
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                                                                           SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP
                                                                                                                                  LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a human beta-integrin CD11c subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d computed that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
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Labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-: diabetees; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11c subunit; rheumatoid arthritis.
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Best Local Similarity 61.0%; Pred. No. 1.5e-275;
Matches 696; Conservative 145; Mismatches 294;
                                                                                                                    Beta-integrin CD11c subunit protein.
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                              AAW65091 standard; protein; 1163
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protein sequence Human

leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; astherosclerosis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11c. Human; macrophage infiltration inhibition; alpha\_d integrin;

Homo sapiens

WO200029446-A1

25-MAY-2000

99WO-US027139 16-NOV-1999;

98US-00193043 99US-00350259 16-NOV-1998; 08-JUL-1999;

(ICOS-) ICOS

Van Der Vieren Gallatin MW,

WPI; 2000-387751/33

Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury

Example 5; Fig 1; 270pp; English

Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11c. This sequence was used in an alignment to identify a novel beta2 integrin alpha approximately 64 identity to the protein sequence of alpha\_d sproximately 64 identity to the protein sequence of alpha\_d. The approximately 64 identity to the protein sequence of alpha\_d. The approximately 64 identity to the protein sequence of alpha\_d. The accions a sproximately 64 identity to the protein sequence of alpha\_d. The class of a clerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (IAD). In addition, anti-alpha d monoclonal antibodies may be used in the system injury. The monoclonal antibodies can also be used to detect and clagnose Crohn's disease

Sequence 1163 AA;

QCDYSTGSCEPIRLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCF 124 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184 67 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQE1VAANQRGSLY Gaps 9 58.4%; Score 3477; DB 3; Length 1163; 61.0%; Pred. No. 1.5e-275; ive 145; Mismatches 294; Indels 6; Best Local Similarity 61.0%; Pr. Matches 696; Conservative 145; Similarity Ŋ 89 œ 65 125 Query Match do ò g

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TLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG 244

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RSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023 PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS 1143 364 365 424 425 485 544 604 484 604 664 902 664 724 724 784 784 844 904 963 545 GEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLVDLAV DPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT 945 HLTC--CSAPVGSQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVGLDRLLLIANVSS SKPPRDHVFQVNNFBALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP RYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP **OTRGGOVSVCPLPRGWR-RWWCDAVLYGEOGHPWGRFGAALTVLGDVNGDKLTDVV1GAP** GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTOVTFFFPLDLSYRKVSTLONQRSQRSW 785 FSFPGLKSLLVGSNLELNAEVMVMNDGEDSYGTTITFSHPAGLSYRYVAEGOKOGOLKSL ENNMPRINKTEFQLELPVKYAVYMVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ SIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS E 1144 E 1143 605 ( 246 306 426 486 999 305 365 425 485 545 505 785 905 1024 1023 1084 1083 1144 1143 725 845 903 964 셤 d ò 셤 엄 요 ò ò Ś 8 셤 ò g ò ద à g 셤 ద ઠે Š ò 셤 ò 8 ò ద ð g 8

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Sequence 10, Appl Sequence 176, Appl Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 3, Appli Sequence 327, App Sequence 4, Appli Sequence 204, App Sequence 3, Appli Sequence 1, Appl Sequence 3 Description US-09-902-481A-1 US-09-912-943-3 1 US-10-144-259-30 1 US-10-144-259-30 US-09-945-265-4 US-09-902-481A-6 US-09-902-481A-5 US-09-902-481A-5 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-09-102-481A-3 US-10-116-275-204 US-09-350-259-4 US-09-350-259-3 SUMMARIES Length 1163 Query Result No.

Sequence 4, Appli	'n	Sequence 2, Appli	99	Sequence 99, Appl	Sequence 53, Appl	23	52,	9	46	e 46	37,	Sequence 37, Appl	Sequence 1212, Ap	Sequence 2, Appli	43	Sequence 130, App	1, 4	1737		1742,	1738	"	1736	1741		Sequence 1871, Ap		174	Sequence 103, App	Sequence 103, App	Sequence 101, App
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58.4	58.0	58.0	57.7	57.7	54.8	54.8	54.6	ゼ	54.4	54.4	53.7	53.7	31.0	26.2	26.2	26.1	26.1	26.1	26.1	26.1	26.1	25.7	25.7	24.6	24.2	22.8	22.8	22.8	20.7	20.7	19.9
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                                                                          GENERAL INFORMATION:

APPLICANT: Callatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Alel Human 2
TITLE BEFERENCE: 27866/35.004
CURRENT PILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER PILING DATE: 1999-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
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EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
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1; Mismatches
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             Sequence 3, Application US/09350259
Patent No. US20020062008A1
GENERAL INFORMATION:
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99.9%; P
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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ORGANISM: Homo sapiens
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APPLICANT: Shimmoka, Motomu
APPLICANT: Shimmoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TILE REPRENCE: A-70586-1/RFT/RMS/RMK
TILE REFRENCE: A-70586-1/RFT/RMS/RMK
CURRENT FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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Publication No. US20030077278A1

GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

APPLICANT: Gallatin, Michael W.

APPLICANT: Gallatin, Michael W.

TITLE OF INVENTION: No. US20030077278A1el Human 2

FILE REPERROCE: 72866/35004

CURRENT APPLICATION NUMBER: US/09/891,943

CURRENT FILING DATE: 1998-11-16

PRIOR PLING DATE: 1998-11-16

PRIOR PLING DATE: 1994-08-05

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 3

LENGTH: 1153

TYPE: PRT

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APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REPERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
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ORGANISM: Homo
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                                                                                                                                                                                                Sequence 30, Application US/10144259
Fublication No. US20030109691A1
GERREAL INFORMATION:
APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui, Amin
APPLICANT: Li, Rui, Amin
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
TILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 09/758,493
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 0;
1; Mismatches
                                                                                                                               APPLICANT: Springer, Timothy A. APPLICANT: Shimaoka, Motomu APPLICANT: Shimaoka, Motomu APPLICANT: Lu, Chafen TITLE OF INVENTION: MODIFIED POLYPEPTIDES STATITE OF INVENTION: MODIFIED POLYPEPTIDES STATITE OF INVENTION: DESIRED CONFORMATION AND FILE REFERENCE: CBN-002CP CURRENT APPLICATION NUMBER: US 60/229,700 PRIOR APPLICATION NUMBER: US 60/229,700 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 4 SEQ ID NOS: 4 SEQ ID NO 4 SEQ ID NO 4 SEQ ID NO 4
                                                                                     Sequence 4, Application US/09945265
Patent No. US20020123614A1
GENERAL INFORMATION:
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Query Match
Best Local Similarity 99.8
Matches 1151; Conservative
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ORGANISM: Homo
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                  GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK
                                                           GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL
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Sequence 6, Application US/09902481A
Publication No. US20030054440A1
September 1 Prognation:
APPLICANT: Springer, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo. Stephen
TILLE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT PILLING DATE: 2001-07-09
PRIOR FILLING DATE: 2001-07-09
PRIOR FILLING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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98.5%; Score 5865; Di
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1132; Conservative 4; Mismatches
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ORGANISM: Artificial sequence
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US-09-902-481A-6
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1036 120 196 180 256 240 300 420 FFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGGGAFVRSQTET 1096 436 496 556 540 919 9 919 99 736 720 796 780 856 840 916 006 QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960 KUEPFEVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQYKDMASEGGPPGAEPQ 1153 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF NFEALKTIONOLREKXFALEGTOTGSSSSFEHEMSOEGFSAAITSNGPLLSTVGSYDWAG GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR RIHFTFKEFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI TDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPRCIEDPVSPIVLRLNF PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDXLTDVAIGAPGEEDNRGAVYLF HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF **QLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV ONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPL** YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNGRSQRSWRLACESASSTEV RINQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 317 121 181 241 301 19 137 197 257 377 437 497 557 421 601 1037 481 617 677 661 737 721 781 841 901 716 196 1021 1097 1081 797 857 917 ò g ò 8 8 g ò 셤 à g ò a ò ద ò 임 g ò д В ò g & g ð g Š д 8 8 8 원 à

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SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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                                                    SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDN1CQDDLS1TFSFMSLDCLVVG
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APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT FILING DATE: 2001-07-09
PRIOR PLLING DATE: 2001-07-09
PRIOR PLLING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4.4
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Pred. No. 0;
8; Mismatches
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US-09-902-481A-4
Sequence 4, Application US/09902481A
Publication No. US20030054440A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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99.1%;
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Matches 1127; Conserv
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        Sequence 5, Application US/09902481A
| Publication No. US2003005440A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Springer, Timothy
| APPLICANT: Shifman, Julia
| APPLICANT: Shifman, Julia
| APPLICANT: Mayo, Stephen
| TILE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| TILE REFERENCE: A-70586-1/RFT/RMS/RMK
| CURRENT FILING DATE: 2001-07-09
| PRIOR FILING DATE: 2001-07-07
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin version 3.1
| SEGION 0.552
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Pred. No. 0;
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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                                                                                                                                                                                                                                                                                  LENGTH: 1137
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         TITLE OF INVENTIVE NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3:
LENGTH: 1137
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                                                                                                                                                                                                                            98.0%;
                                                                                                                                               TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic US-09-902-481A-3
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Best Local Similarity 98.8
Matches 1123; Conservative
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RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI
                                                                   241 TDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN
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                                                                                                                    GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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             TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF

US-09-902-481A-3
; Sequence 3, Application US/09902481A
; Sequence 3, Application US/09902440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Wolcomu
; APPLICANT: Shifman, Julia

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APPLICANT: Aziz, Natasha
APPLICANT: Glabburg, Wendy M.
APPLICANT: Glabburg, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/7123,860
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                      GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
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                                                                          LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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; Publication No. US20040253606A1
; GENERAL INFORMATION:
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Sequence 204, Application US/10116275

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                    GPREFNVIVIVINDGEDSYRIQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESASŚTEV
                                                                          SCALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTEP
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Matches 699; Conservative 139;
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US-10-116-275-204
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                                                                                                                                                                                                         TQFSLMQFSNKFQTHFTFEEFRRTSNPLSLLASVHQLQGFTYTATAIQUVVHRLFHASYG
   845 HLTCDSAPVG--SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS
                                     ENNMPRINKTERQLELPVKYAVYMVYTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
                                                                                                                                                                                                                                                          PGOGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
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                                                                         ENNIPRISKTIFOLELPVKYAVYTVVSSHEQFIKYLNFSESEEKESHVAMHRYQVNNLGQ
                                                                                                           RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                                                   SIAVCORIOCDIPFFGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL
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Best Local Similarity 61.0%; Pred. No. 5.5e-278;
Matches 696; Conservative 145; Mismatches 294; Indels
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Alel Hum
FITLE REPEBROCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
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EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOUTWARE: PATENTING DATE: 1997-10-03
SEQ ID NO 4
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Patent No. US20020062008A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
                                                    NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-327
                                                                                        SEQ ID NO 327
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Publication No. US20030077278A1
GENERAL INCORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278A1el Human
FILE REFERENCE: 27866/35004
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RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE
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                                                                                                                                                                                                                                                                                                              tch 58.4%; Score 3477; DB 10; al Similarity 61.0%; Pred. No. 5.5e-278; 696; Conservative 145; Mismatches 294;
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR PLILNG DATE: 1998-11-16
PRIOR PLILNG DATE: 1994-08-05
PRIOR PLILNG DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR PILING DATE: 1994-12-21
PRIOR PILING DATE: 1994-12-21
PRIOR PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN VET: 2.0
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US-09-891-943-4
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LLGSRW-E11QTVPDATPECPHQEMDIVFL1DGSGS1DQNDFNQMKGFVQAVMGQFEGTD
                                                                                ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA
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                          TLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG
                                           LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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                          845 HLTC--CSAPVGSQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVGLDRLLLIANVSS
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ENNIPRISKTIFQLELPVKYAVYIVVSSHEQFTKYLNFSESEERESHVAMHRYQVNNLGO
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                                                                RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS
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Best Local Similarity 59.9%; Pred. No. 6.4e-276;
Matches 683; Conservative 163; Mismatches 287; Indels
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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20020062008A1el Humirit RIE REPERRICE: 27866/35004
CURRENT FILING DATE: 1999-07-08
BARLIER APPLICATION NUMBER: 09/193,043
BARLIER FILING DATE: 1998-11-16
BERLIER FILING DATE: 1994-08-05
BARLIER FILING DATE: 1994-12-21
BARLIER PILING DATE: 1994-12-21
BARLIER FILING DATE: 1994-12-21
BARLIER FILING DATE: 1994-12-21
BARLIER FILING DATE: 1994-12-21
BARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PARCHIN VET: 2.0
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Sequence 43, Appl
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(c) 1993 - 2005 Compugen Ltd.
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US-08-266-889-3
US-08-485-618-3
US-08-605-672-3
US-08-605-672-3
US-08-43-363-3
US-09-43-363-3
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US-08-362-62-4

US-08-485-618-4

US-08-362-62-4

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US-08-139-043-4

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
                                                                                                                                                                                                                                                                                             Sequence:
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Sequence 3, Application US/08173497;
Sequence 3, Application US/08173497;
Sequence 3, Application US/08173497;
Sequence 1 NFORMATION:
TITLE OF INVENTION: Subunit
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
CORRESPONDENCE ADDRESS: 3
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STREET: 111inois
COUNTRY: USA
ZIP: 60606-6402
COUNTRY: USA
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: PROPS/MS-DOS
SOFTWARE PREADILIN Release #1.0, Version #1.25
CURRENT APPLICATION UMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 437
APPLICATION: MADDRESSER
COMPANDENT VARDANT B 1; Length 1153; Indele US-08-362-652-2 US-08-605-672-2 US-08-943-234A-2 US-09-193-043-2 US-09-193-043-2 US-09-193-043-2 US-08-485-618-99 US-08-485-618-99 US-08-943-363-99 US-08-943-363-99 US-09-193-043-99 US-09-135-293A-99 US-09-135-253-99 US-09-350-259-99 US-09-350-253-3 US-08-485-618-53 US-08-485-618-53 US-08-485-618-53 100.0%; Score 5953; 99.9%; Pred. No. 0; tive 1; Mismatches ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPEX: 312-474-6448
TELEX: 32-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS: ALIGNMENTS 1153 amino acids Best Local Similarity 99.9 Matches 1152; Conservative TYPE: amino acid STRANDEDNESS: single MOLECULE TYPE: protein linear 558.00 568.00 568.00 568.00 569.00 US-08-173-497-3 US-08-173-497-3 34444 3444 3444 3444 3444 3444 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 3433 343 3433 343 343 343 343 343 343 343 343 343 343 343 343 343 343 343 Query Match à

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Sequence 2, Sequence 2,

US-09-350-259-4 US-08-173-497-2 US-08-286-889-2

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                                                                                                                                                                                                                                                                          SEE: Marshall, O'Toole, Gerstein, Murray (1: 233 South Wacker Drive, 6300 Sear Tower Chicago
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 0;
1; Mismatches
                                                                                                                                                                                     APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Williams Jr., Joseph A.
RECISTRATION NUMBER: P38,659
REPERNICE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                             Sequence 3, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
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99.9%; F
1141 MMSEGGPPGAEPQ 1153
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                   1141 MMSEGGPPGAEPO 1153
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 1152, Conservative
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                                     GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGFTVHQTCSENTYVK 120
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               GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHOTCSENTYVK
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233 South Wacker Drive, 6300 Sear Tower
                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 1-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ur., JOSEPPh A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         US/08/485,618
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TELEFAX: 312-474-0448
            CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 1152; Conservative
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; MOLECULE TYPE: protein
US-08-485-618-3
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                                      LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP
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                                                                                 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
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Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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US-08-485-618-3
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           APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY, AGBNI INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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Best Local Similarity 99.9
Matches 1152; Conservative
 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             amino acid
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STATE: 111inois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Patent No. 5766850;
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2;
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, M
STREET: 233 South Wacker Drive, 6300 Sear
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                          STRDRLREGOIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP
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Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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CITY: Chicago
STATE: 1111nois
COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 5953;
99.9%; Pred. No. 0;
iive 1; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERNCE/DOCKET NUMBER: 27866/32684
TELECOMMINICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.9
Matches 1152; Conservative
                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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NVTSENNMPRTNKTEFQLELPVKXAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960
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1; Mismatches
                                                                                               Score 5953;
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LENGTH: 1153 amino acids
                                                                                                              Best Local Similarity 99.9
Matches 1152; Conservative
                             single
                                                     MOLECULE TYPE: protein
              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                            Similarity
                                                                   US-08-482-293A-3
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LSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS 840
                 781 LSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                                                         QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
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STREET: 233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482.291A
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08482293A, Patent No. 5831029, GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael, APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5831029e1 Human, NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 21-DEC-1994
ATTORNEY/ABENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-482-293A-3
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ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300 NTIASKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360

480 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480 LGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP

900 960 DLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK

STRDRLREGGIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP

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STRDRLREGQIOSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP NCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD

LSITESEMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS

**QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA** 

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LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
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                                                                                           GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120
                                                                                                                        61 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAAATTSPPQLLACGPTVHQTCSENTYVK 120
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                                          1 MALRVILLTALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
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NVTSENNMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960
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Fatent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
TTATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                          VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVF
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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99.9%; Pred. No. 0;
iive 1; Mismatches
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PRIOR APPLICATION DATA:
PRIOR DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams JT., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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TELEFAX: 312-474-0448
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Best Local Similarity 99.9
Matches 1152; Conservative
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REPRENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT PILING DATE: 2000-10-13
PRIOR PRILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/05,672
PRIOR APPLICATION NUMBER: 08/05,672
PRIOR APPLICATION NUMBER: 08/13,497
PRIOR FILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/36,652
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR PILING DATE: 1994-12-21
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
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      TLLPGOGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140
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ive 1; Mismatches
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Sequence 3, Application US/09193043

Sequence 3, Application US/09193043

Sequence 3, Application US/09193043

GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

TITLE OF INVENTION: NO. 6251395e1 Human 2

FILE REFERENCE: 27866/35004

CURRENT FILING DATE: 1993-11-16

SEARLIER APPLICATION NUMBER: US/09/193,043

CURRENT FILING DATE: 1993-12-23

EARLIER FILING DATE: 1993-12-23

EARLIER PELING DATE: 1994-12-21

EARLIER PELING DATE: 1994-12-21

EARLIER PELING DATE: 1994-12-21

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EARLIER PILING DATE: 1994-12-3

EARLIER PILING DATE: 1994-12-3

SADFWARE: PELING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTING UNDER: US/991363

SEQUID NO 3

LENGTH: 1153
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Matches 1152; Conservative
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Voeren, Monica
ITILE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350, 259
CURRENT FILING DATE: 1999-07-08
EARLIER FILING DATE: 1999-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER PELING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
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Patent No. 6620915
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Matches 1152; Conservative
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ORGANISM: Homo sapiens
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Matches 1152; Conservative
                              TYPE: PRT
CAGANISM: Homo sapiens
US-09-688-307A-3
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LENGTH: 11
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASSESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-UNN-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-UNN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-UNN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-UNN-1981
APPLICATION NUMBER: 07/212,573
FILING DATE: 18-UN-1988
APPLICATION NUMBER: 07/212,573
FILING DATE: ABANGMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 5922.5; Pred. No. 0; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                        NAMB: Freeman, John W. REGISTRATION NUMBER: 29,066
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INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
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Matches 1149; Conservative
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FRAGMENT TYPE: internal
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Batent No. 5877275

GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
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Pred. No. 0;
1; Mismatches
                          ATTORNEL FOLLS.

NAME: JOHN W. Freeman
REGISTRATION NUMBER: 29,066
REFRERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-806
                                                                                                                                                       43:
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.7%;
Matches 1149; Conservative 1
 FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
                                                                                                                TELEFAX: (617) 542-8906
TELEX. 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1152
                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
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TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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COUNTRY: U.S.A.
2110-2804
CONPUTER: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPATIOR SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
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301 NTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT
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Patent No. 5877275

GENERAL INFORMATION:

APPLICANT: Arnaout, M. Amin

TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

STATE: MA
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                                                                         QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
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LSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                                                        QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
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Patent No. 5424399

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FILING DATE: 16-JUM-1993

PRIOR APPLICATION NUMBER: 539,842

FILING DATE: 10-JUM-1990

APPLICATION NUMBER: 212,573

FILING DATE: 28-JUM-1990

FILING DATE: 28-JUM-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 5922.5;
; Pred. No. 0;
1; Mismatches
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Best Local Similarity 99.7%;
Matches 1149; Conservative
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                                                    505 GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD
                                                                                                                                                                             565 RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE
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ZIP: 02110-2804
COMPUTER READBALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OMPRTER: MS MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
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GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENT
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
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STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OSTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              00786/068003
                                                                                                                                                                                        APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 1163 amino acids
amino acid
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-476-062A-44
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                                                                                                                                                                                                                                                                                                       TLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
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                                                                                                                                                                        Gaps
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9
                                                                                                                                                    Length 1163;
                                                                                                                                                                      Indels
                                                                                                                                                  Query Match 58.8%; Score 3500; DB 5; Best Local Similarity 61.3%; Pred. No. 2.3e-279; Matches 699; Conservative 139; Mismatches 297;
                29,066
ER: 00786/267001
      NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0078(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERX: 6017) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                    TYPE: amino acid
;
STRANDEDNESS:
;
TOPOLOGY: linear
PCT-US96-01314-44
                                                                                            LENGTH: 1163
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                                                                                      845 HLTCDSAPVG--SQCTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS
                                                                                                                                                                         ENNTPRISKTTFQLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQ
                                                                                                                                                                                                                                 RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                                                                                                                                                                                    SIAVCORIQCDIPPFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL
                                                              RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS
                                                                                                                                                 ENNMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
```

Search completed: January 13, 2005, 15:34:33 Job time : 61.4108 secs

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version 5.1.6
- 2005 Compugen Ltd.
 GenCore (c) 1993 .
            Copyright
```

- protein search, using sw model OM protein January 13, 2005, 15:03:32 ; Search time 5.47465 Seconds (without alignments) 3321.665 Million cell updates/sec Run on:

RWHU1B-B\_COPY\_144\_332 Perfect score:

966 1 CPQEDSDIAFLIDGSGSIIP......FQVNNFEALKTIQNQLREKX 189 **BLOSUM62DX** Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	,	Query	Query		!	
00	Score	Match	Length	BB	ID	Descripti
-	996	100.0	1	-	RWHU1B	cell surf
~	746	77.2	1153	~	800551	leukocyte
m	540	55.9		Н	RWHU1C	cell surf
4	328	34.0		~	A53213	integrin
ហ	287.5	29.8	1170	~	803308	cell surf
9	261	27.0		~	156126	lymphocyt
7	243	75.1		c	99966	0001:4300

	Description	cell surface glyco	ocyte surf	cell surface glyco	grin a]	cell surface glyco		_	cartilage matrix p	matrix	1pha 1	collagen alpha 1(X	alpha 1	collagen alpha 1(X	integrin alpha-1 c	hypothetical prote	integrin alpha-1 -	integrin alpha-1 c	hypothetical prote	type XII collagen	collagen alpha 1 (V	collagen alpha 3(V	collagen alpha 3(V	alpha	alph	o	hypothetical prote	٦,	15	complement factor
	ΩI		800551	RWHU1C	A53213	803308	156126	A33809	S66522	A37979	A40020	A45974	S31212	S78476	A45226	S42373	A55348	A35854	T46488	151027	A54849	CGHU3A	A37797	145914	A33998	S44142	T23760	A40970	326	080
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٠. م	Match	100.0	77.2	55.9	34.0	29.8	27.0	25.1	24.3	24.0	22.3	22.2	22.2	22.2	21.5	21.5	20.4	19.9			18.1				•		15.1			14.1
	Score	996	746	540	328	287.5	261	242	235	232	_	14.	14.	14.	207.5	07.	97.	192.5		188	174.5	164	162	159	154	149	146	143	40	136.5
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712	2813	191	1029	1022	238	917	1018	724	918	1019	427	414	764	567	13055
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5.5	132	127.5	125.5	124.5	122.5	122.5	122.5	119.5	118.5	118	115.5	113.5	112	109.5	109.5
134		٠.													

## ALIGNMENTS

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Nighternate glycoprotein CD11b precursor [validated] - human
Nighternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Maceukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004
Cipacession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Cham. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)

A; Reference number: A31108; MUID:88315033; PMID:2457584 A; Accession: A31108

A.Accession: Aillow
A.Molecule type: mRNA
A.Residues: 1-1153 (COR)
A.Accession: Aillow
A.Accession: Aillow
A.Accession: Aillow
A.Accession: Aillow
A.Accession: Aillow
A.B. Gupta S.K.; Pierce was confirmed by protein sequencing
B.Acraout, M.A.; Gupta S.K.; Pierce was confirmed by protein sequencing
B.Acraout, M.A.; Gupta S.K.; Pierce was confirmed by protein sequencing
B.Acraout, M.A.; Gupta S.K.; Pierce was confirmed by protein by a coll Biol. 106, 2153-2158, 1988
A.F. Coll Biol. 106, 2153-2158, 1988
A.F. Reference number: A28915, WIDTO 8827215, PMIDD:244991
A.R. Residues: 1-499,501-786, P., 967-1153 ARNA
A.Residues: 1-499,501-965, P., 967-1153 ARNA
A.Residues: 1-499,501-786, P., 967-1153 ARNA
A.Residues: 1-499,501-786, P., 967-1153 ARNA
A.Residues: 1-409,501-786, P., 967-1153 ARNA
A.Residues: 1-409-501-786, P., 967-1153 ARNA
A.Residues: 1-409-501-786, P., 967-1153 ARNA
A.Residues: 1-409-501-786, P., 967-1153 ARNA
A.Residues: 1-50-501-786, P., 967-1154, P., 967-116, P., 96

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N;Alternate names: complement-3 receptor alpha chain
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A, Molecule type: protein

A, Molecule type: protein

A, Residues: 17-31 (-21E).
A, Residues: 17-31 (-21E).
A, Residues: 17-31 (-21E).
B, BS-2510, 1925.
B, BS-2510, 1925.
B, MUD: 9144986; PMID: 1346576
A, Reference number: 152567; MUD: 92144986; PMID: 1346576
A, Reference number: 152567; MUD: 92144986; PMID: 1346576
A, Reference number: 152567; MUD: 92180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9553219
A, Rocel references: GB: M84477; NID: 9180184; PIDN: AAA51960.1; PID: 9180184; PIDN: AAA5196019; CB: M84477; MAD: 9180184; PIDN: AAA5196019; GB: M84477; MAD: 9180184; PIDN: AAA5196019; GB: M84477; M94499; M9499101; GB: M844998; M9499101; GB: M949994; M9499; ,Note: part of this sequence was confirmed by protein sequencing
R,Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1933
A,Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in n during evolution.
A,Reference number: A46526, MUID:93123748; PMID:8419480
A,Accession: A46526
A,Accession: A46526
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A Molecule type: DNA

A Molecule type: DNA

A Molecule type: 1-1153 <FLE>

A Molecule type: 1-1153 <FLE>

A Molecule type: 1-1153 <FLE>

A Molecule the last three bases of intron 13, CAG, are included in some but not all mature

A Note: the last three bases of intron 13, CAG, are included in some but not all mature

A Note: sequence extracted from NCBI backbone (NCBIP:121963)

A Molecule sequence of the sequence (NCBIP: A Transout, M.A.

Biochim. Biophys. Acta 874, 368-371, 1986

A Mittle: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp.

A Molecule number: A90664; MuID:87076671; PMID:3539202
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S00551
Jeukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation Molecule type: DNA
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hes 188; Conservative
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C. Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol C; Superfamily: cell adhesion; glycoprotein; transmembrane protein C; Keywords: cell adhesion; glycoprotein; transmembrane protein P:1-16/Domain: signal sequence #status predicted <SIG> F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2> F:1106-1129/Domain: transmembrane #status predicted <TWM>
                                                                                               the leukocyte p150,95 molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Call Surface glycoprotein CD11c precursor - human NiAlternate names: leukocyte adhesion receptor p150,95 alpha chain C,Species: Homo sapiens (man)
C;Species: A36584, A3554013z, U.; Springer, T.A.
U. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Roches: erratum
A;Accession: A36584
A;Holccule type: DNA
A;Residues: 1-1163 <COR>
A;Cross-reference: UNIPPUT: D00702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 CPQQESDIVFLIDGSGSINNIDFQKMKEFVSTVMEQFKKSKTLFSLMQYSDEFRIHFTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00551; 159078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPOEDSDIAFLIDGSGSILPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

77.2%; Score 746; DB 2;
Best Local Similarity 77.8%; Pred. No. 8.6e-56;
Matches 147; Conservative 20; Mismatches 22
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C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 20-Feb-1990 #47565; A47565; A48759; S36044
R;Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A;Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit: A;Reference number: S03308; MUID:89139587; PMID:2537322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1170 < LAR>
A; Cross-references: UNIPROT: P20701; UNIPROT: Q9UBC8; EMBL: Y00796; NID: g31421; PIDN: CAA687;
A; Cross-references: UNIPROT: P20701; UNIPROT: Q9UBC8; EMBL: Y00796; NID: g31421; PIDN: CAA687;
A; Note: part of this sequence was confirmed by protein sequencing
R; Cornwell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl.: Acad. Sci. US.A. 90, 4221-4225, 1993
Proc. Natl.: Acad. Sci. US.A. 90, 4221-4225, 1993
A; Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pron
A; Reference number: A47458; MUID: 93248261; PMID: 8097887
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Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A;Title: Identification of cell-specific and developmentally regulated nuclear factors the A;Reference number: A47565; MUID:93281759; PMID:8099450
A;Accession: A47565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell surface glycoprotein CD11a precursor - human
N;Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
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Biol. Chem. 268, 19385-19311, 1993
;Title: Characterization of the CD11a (alphal, LFA-lalpha) integrin gene promoter.;Reference number: A48759; MUID:93374910; PMID:8103515
                                                                              201 TEIAIILDGSGSIDPPDFQRAKDFISNWMRNFYEKCFECNFALVQYGGVIQTEFDLRDSQ 260
                                                                                                                                                                                                                                321 NLTTVINSPKMQGVERPAIGVGEEPKSARTARELNLIASDPDETHAFKVTNYMALDGLLS 380
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                                                                                                                                                                                   64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL
                                            6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL--KKSKTLFSLMQYSEBFRIHFTFKBFQ
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Residues: 1-20 <COR>
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Residues: 1-20 <SHE>
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Residues: 1-20 <NUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 QLR 186
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Best Local S
Matches 62
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A;Molecule type: DNA
A;Residues: 1-834 <CO2>
A;Residues: 1-834 <CO2>
A;Note: this sequence has been revised in reference A36584
B;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A;Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte A;Reference number: S00864; MUID:88166645; PMID:3327687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:ITGAX; CD11C
A;Cross-references: GDB:119758; OMIM:151510
A;Cross-references: GDB:119758; OMIM:151510
C;Map position: 16p11.2-16p11.2
C;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein (D11b; von Willebrand factor type A repeat home C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG>P:1-19/Domain: signal sequence glycoprotein (D11c #status predicted <MAT>F;20-1103/Domain: extracellular #status predicted <EXT>F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4>F;108-113/Domain: theracellular #status predicted <INT>F;113-115/Domain: intracellular #status predicted <INT>F;113-115/Domain: intracellular #status predicted <INT>F;113-115/Domain: intracellular #status predicted <INT>F;61,89;392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre
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A, Map position: 17p13
C, Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
P;199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
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C;Species: Homo sapiens (man)
C;Date: 19-OCT-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C;Accession: A51213
R;Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
A;Fitle: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit.
A;Reference number: A53213; MUID:94164962; PMID:8119947
                                                                                                                                                                                                                                                                                                                      A;Residues: 1-755, L',757-1163 <CO3>
A;Cross-references: CB:M81655; EMBL:V00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Cross-references: CB:M81655; EMBL:V00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Croment: A common beta chain (CDB) forms a heterodimer with CD11b to form Mac-1 on C;Comment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,
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Cross-references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245
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Matches 71; Conserv
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A; Residues: 1-1179 cs
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                                                                                                             A, Accession: A26364
A, Molecule type: mRNA
A, Residues: 78-493 <ARG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-500 <ASZ>
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Best Local S:
Matches 56
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C,Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homc
F,151-315/Domain: von Willebrand factor type A repeat homology <VWAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-1163 <RES>
;Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156126 #sequence_revision 1.A.
J. Immunol: 147, 369-374, 1991
J. Immunol: 147, 369-374, 1991
A;Title: Cloning of the murine 1ymphocyte function-associated molecule-1 alpha-subunit A;Reference number: 156126, MUID:91268576; PMID:2051027
A;Accession: 156126
A;Accession: 156126
A;Molecule type: mRNA
A;Residues: 1-1163 <-RESS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
267
                                                                                                                                                                                                                                          268 TDSGNIDAAKD----IIRYIIGIGKHFQTKESQETLHKFASKFASEFVKILDTFEKLKD 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                          EPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156126
lymphocyte fuction-associated molecule-1-alpha - mouse
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DTFEKLKDLFTDLQRRI 329
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32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                LFTELOKKI 331
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Best Local Similarity
Matches 63; Conserv
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A;Cross-references: UNIPROT:P51942; EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163.6; G;Genetics:
A;Genetics:
A;Gene: CMP
C;Genetics:
A;Gene: CMP
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repective C;Superfamily: dignal sequence #status predicted <SIG>P;0-29/Domain: cartilage matrix protein #status predicted <MAT>P;31-20/Domain: von Willebrand factor type A repeat homology <VWAI>P;231-266/Domain: EGF homology <EGF>P;77-441/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                                                                                                  A;Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat; Sip-7-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F;225-260/Domain: EGF homology <EGF>
F;225-260/Domain: von Willebrand factor type A repeat homology <VWA2>
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R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Accession: S66522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPNPRSLVKPITQLLGRTHTATGIRKVVRELPNITNGARKNAFKILVVITDGEKFGDPLG 124
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C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTL--FSLMQYSEEFRIHFTFKEFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F. Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A;Title: Structural features of cartilage matrix protein deduced from cDNA. A;Reference number: A26364; MUID:87092429; PMID:3025875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS--KTLFSLMOYSEEFRIHFTFKEFQN
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29.5%; Pred. No. 1.9e-12;
ive 45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 25.1%; Score 242; DB 2; Local Similarity 31.2%; Pred. No. 4.8e-13; hes 59; Conservative 39; Mismatches 73;
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A,Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, R,Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A,Fitle: Type XII collagen. A large multidomain molecule with partial homology to type IN A,Reference number: A34485; MUID:90062079; PMID:2584192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 2772-2792,2846-2873 <GOR2>
R,Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A,Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA cl
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A; Rsbullet, B. ), van der Rest, M.
R; Dublet, B.), van der Rest, M.
A; Tatle: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-c
A; Rteference number: S22254; MUID: 88087065; PMID: 3121603
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1.23/commain: signal sequence #status predicted <2450.
1.24-3124/product: collagen alpha 1(XII) chain #status predicted <4MI>
1.24-114/Domain: IIIA #status predicted <IIIA>
1.24-114/Domain: IIIA #status predicted <IIIA>
1.31-301/Domain: von Willebrand factor type A repeat homology <VWAl>
1.317-301/Domain: IIIB #status predicted <IIIB>
1.32-425/Domain: IIIB #status predicted <IIIB>
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Buchen. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
A;Reference number: S23814; MUID:92362621; PMID:1323460
     A;MOlecule type: mRNA
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1;
                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A34485
A,Molecule type: mRNA
A,Residues: 2456-2758, A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A,Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A,Accession: B34485
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A;Residues: 2960-2976, F',2978-3074,'AG' <GOR3>
A;Cross-references: EMBL:M7375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A;Note: this sequence has been revised in reference A34485
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Title: The two splice variants of collagen XII share a common 5'
Reference number: S28811; MUID:93042014; PMID:1420368
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Residues: 2811-2812,'T',2814,'R',2816-2841;3002-3014 <DUB>
Trueb, J.; Trueb, B.
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Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
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A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g
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Cartilage matrix protein precursor - human

C;Space: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004

C;Accession: A37979; B37979

A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix
A;Reference number: A37979; MUID:91060568; PMID:2246248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 -- ODYINDAAKKAKDLGFKMFAVGVGNAV----EDELREIASEPVAEHYFYTADFKTIN 441
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F;221-238,234-247,249-262/Disulfide bonds: #status predicted
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F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
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24.0%; Score 232; DB 2; Length 496;
Best Local Similarity 29.5%; Pred. No. 3.5e-12;
Matches 56; Conservative 43; Mismatches 73; Indels
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A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
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A;Accession: B37979
180 TIQNQLREKX 189
                                                                                            446 QIGKKLQKQI 455
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61; Conservative
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Best Local Similarity
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F;1756-1838/Domain: fibronectin type III repeat homology <FN3M>
F;1947-1928/Domain: fibronectin type III repeat homology <FN3N>
F;1937-2019/Domain: fibronectin type III repeat homology <FN3D>
F;2028-2110/Domain: fibronectin type III repeat homology <FN3D>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3D>
F;2207-2224/Domain: fibronectin type III repeat homology <FN3D>
F;2207-2224/Domain: fibronectin type III repeat homology <FN3D>
F;2438-2440/Region: cell adhesion #status predicted
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F;2509-2750/Domain: ollagenous COL2 #status predicted <COL2>
F;2809-2901/Pomain: collagenous COL2 #status predicted <COL2>
F;2454-3048/Domain: collagenous COL1 #status predicted <COL2>
F;2449-3124/Domain: collagenous COL1 #status predicted <COL1>
F;34049-3124/Domain: non-collagenous COL1 #status predicted <COL1>
F;34049-3124/Domain: non-collagenous NC1 #status predicted <COL1>
F;32040-3124/Domain: non-collagenous NC2 #status predicted <COL1>
F;32040-3124/Domain: non-collagenous NC3 #status predicted <NC2>
F;32040-3124/Domain: non-collagenous NC3 #status predicted <NC3>
F;32040-3124/Domain: collagenous NC3 #status predicted <NC3>
F;32040-3124/Domain: non-collagenous NC3 #status predicted <NC3>
F;32040-3124/Domain: non-collagenous NC3 #status predicted <NC3>
F;32040-3124/Domain: collagenous NC3 #status predicted <NC3>
F;32040-3124/Domain: non-collagenous NC3 #status predicted <NC3
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N'Alternate names: undulin
C;Species Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; $22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 GYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQEINTIASKPPRDHVFQVNNFEALK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
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A.Molecule type: mRNA
A.Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A45974
A;Status: preliminary
A;Nolecule type: minA3, protein
A;Residues: 1-1747 «GER»
A;Cross-references: UNIPROT:P32018
A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
B;Apte, S.S.
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Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 30.6%; Pred. No. 9.9e-10; 57; Conservative 37; Mismatches 74;
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                                                                                                                                                         F;2119-2199/Domain: f
F;2207-2294/Domain: f
F;2325-2490/Domain: v
F;2438-2440/Region: c
F;2509-2750/Domain: c
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R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F
Bur. J. Biochem. 201, 333-338, 1991

A;Ritle: Cloning of a cDNA for a new member of the class of fibril-associated collagens v
A;Reference number: S17035; MUD:92037585; PMID:1935930

A;Reference number: S17035

A;Molecule type: mRNA
A;Residues: 1472-1659 <GGR1>
A;Accession: S20833

A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GGR2>
A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GGR2>
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F;40-204/Domain: von Willebrand factor type A repeat homology <WA1>
F;236-317/Domain: fibronectin type III repeat homology <RN3D>
F;236-317/Domain: fibronectin type III repeat homology <RN3D>
F;207-591/Domain: fibronectin type III repeat homology <RN3D>
F;207-591/Domain: fibronectin type III repeat homology <RN3C>
F;1111-1352/Domain: fibronectin type III repeat homology <RN3C>
F;1111-1352/Domain: fibronectin type III repeat homology <RN3C>
F;1111-1352/Domain: non-collagenous NC2 #status predicted <NC2L>
F;1111-1353/Domain: non-collagenous NC2 #status predicted <NC2L>
F;1111-1353/Domain: triple helical domain COLI #status predicted <NC2L>
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A;Residues: 1-1857 ~ WAE>
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Cross-references: EMBL:X70792; NID:g288874; PID: g288875
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gene
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S11212
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Ba.cochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; WUID:93185668; PMID:8444186
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
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tive 31; Mismatches 85; Indels
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A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F;754-793/Domain: fibronectin type II repeat homology <2F1>
F;1201-1244/Domain: EGF homology <EGF>
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A45226
A5 pecies: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30.Apr.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: A45226
R; Bitlesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2389-2396, 1993
A; Title: Expression of native and truncated forms of the human integrin alpha 1
A; Reference number: A45226; MuID:93155124; PMID:8428973
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-1151 cBRI>
A; Cross-references: UMTRROT:P56199
A; Residues: 1-1151 cBRI>
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                                                                                              118 KFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEA 177
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C;Species: Caenorhabditis elegans
C;Date: 07-Oct.1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C;Accession: S42373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1151;
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A;Residues: 1-3051 <SMI>
A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
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29.8%; Pred. No. 1.2e-09;
tive 39; Mismatches 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.84
Matches 57; Conservative
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Matches 63,
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Fil-28/Domain: signal sequence #status predicted <510>
Fil-28/Domain: signal sequence #status predicted <510>
Fil-29-108/Domain: fibronectin type III repeat homology <FN3A>
Fil-29-10/Domain: fibronectin type III repeat homology <FN3B>
Fil-252/Domain: fibronectin type III repeat homology <FN3D>
Fil-252/Domain: fibronectin type III repeat homology <FN3D>
Fil-29-10/Domain: fibronectin type III repeat homology <FN3B>
Fil-20-1009/Domain: fibronectin type III repeat homology <FN3B>
FN3B-1009/FN3B-1009/FN3B-1009/FN3B-1009/FN3B-1009/FN3B-1009/FN3B-1009/FN3B-1009/FN3B-
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A,Residues: 1-1888 cTRU>
A,Cross-treferences: UNIPROT:P32018; EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:92888
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036 CKAAKADLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEF 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 TFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S78476; S31211
R;Trueb, B.
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F;832-914/Domain: fibronectin type III repeat homology <FN3G> F;922-1009/Domain: fibronectin type III repeat homology <FN3H> F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                  ; Score 214.5; DB 2; Length 1857;
; Pred. No. 5.7e-10;
31; Mismatches 85; Indels 11;
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32.4%; Pred. No. 5.8e-10;
iive 31; Mismatches 85
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A;Reference number: S78476
A;Accession: S78476
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A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: EMBL:X70793
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22.2%;
Best Local Similarity 32.4%;
Matches 61; Conservative 3:
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                                                                           623 AILLTDGRSQDNVTGPAD---SARKLSINTFAIGVTDHVLA---SELESIAGSPNR--W 673
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"CDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
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MEDLINE-89098893; Pubmed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
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evolution
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Q6KA<u>S</u>4
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Q96dm8 homo sapien
Q96hb1 homo sapien
Q99k64 mus musculu
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gallus gall
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MEDLINE=88190151; PubMed=2833753;
Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
Arnaout Cloning of the alpha subunit of human and guinea pig
"Molecular cloning of the alpha subunit of human and guinea pig
leukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

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J. Biol. Chem. 263:12403-12411(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88257215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Manino acide acquence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
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P11215;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1986 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 45, Last annotation update)
101-OCT-2004 (Rel. 45, Last annotation update)
101-OCT-2014 (Rel. 45, Last annotation update)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            Q8c270 m
Q951i2 k
P51942 m
Q80vm5 m
P21941 k
Q96dt1 k
                                    Q98tf0
P05099
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                                                            CAMA CHICK
Q8C270
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CAMA MOUSE
Q80VNS
CAMA HUMAN
Q96DFI
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Q96DM8
Q96HB1
Q99K64
    AAQ90015
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PRINTS: PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00191; Int_alpha; 5.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0244; WWPA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0008305; C:integrin complex; TAS. GO; GO:0007155; P:cell adhesion; TAS. Interpro; PRR006413; Integrin_alpha. Interpro; IPR002035; VWF.A.
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Pfam, PF001837; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PDB, 1A8X; Model; Ø=17-1152.
PDB, 1BHO; X-ray; 1/2=-.
PDB, 1BHO; X-ray; 1/2=-.
PDB, 1IDN; X-ray; 1/2=-.
PDB, 1IDN; X-ray; 0=140-331.
PDB, 1IDN; X-ray; Ø=140-331.
PDB, 1MU; X-ray; Ø=143-334.
PDB, 1NWZ; X-ray; Ø=144-337.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-345.
PDB, 1NWZ; X-ray; A=140-345.
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DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

WILLARITY: Conclust to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl1b.htm".
                                                                                                                                                                                                                                                                                                                          MEDIANE=87076671; PubMed=3539202; MEDIANE=87076671; PubMed=3539202; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; Pierce M.W., Respuence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE=96363671; PubMed=8747460;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee J.O., Rieu P., Arnaout M.A., Liddington R.; Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98362595; PubMed-9687375; Baldwin B.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Baldwin B.T., Sarver R.W., Bryant G.L. Jr., Heinrikson R.L., Faizel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.B., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation model
                                 SEQUENCE OF 1-9 FROM N.A.
MEDLINE-92073318; PubMed=1683702;
Shellay C.S., Armaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
                                                                                                                                                                                                         MEDLINE-92144986; PubMed-1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
 Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95171458; PubMed=7867070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 3:1333-1340(1995).
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                                                                                                                                                                           SEQUENCE OF 1-9 FROM N.A.
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REQUENCE FROM N.A. (ISOFORM 2).

REQUENCE FROM N.A. (ISOFORM 2).

REQUENCE FROM N.A. (ISOFORM 2).

REQUENTES 3354683; PubMed=12466851; Ddachi J., Bono H., Kondo S.,

RA MEDINTES-2354683; PubMed=12466851; Ddachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Hadarelli R., Hill D.P., Bult C., Hume D.A., Chordench J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Chordench J.,

RA Baldarelli R., Marsic V., Chothia C., Corbonia C., Corbonia C.,

RA Balake J.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gløsi C., Godzík A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., Lyons P.A.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Martais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Peavan W.J., Pertea G.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Varardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wat S.,

RA Van Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatuu N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

RA Hara A., Hashizume W., Imoteani K., Ishii Y., Ichh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa T.,

RA Hara A., Hashizume W., Imoteani K., Ishii Y., Iloh M., Kagawa I.,

RA Wannishin A., Ysonlino M., Waterston R., Lander E.S., Rogers J.,

RA Hara A., Hashizawi Y.,

RA Hara A., Handerston R., Lander E.S., Rogers J.,
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                             ITAM MOUSE STANDARD; PRT; 1153 AA.
P05555, QBCA73;
P01-NOV-1988 (Rel. 09, Created)
O1-NOV-1988 (Rel. 17, Last sequence update)
O5-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 11-45 FROM N.A.
STRAIN=BALB/c; TISSUE=Spleen;
MEDLINE=86287312; PubMed=2942940;
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MEDLINE=88312584; PubMed=3044779;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                              Length 1152;
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80.4%; Pred. No. 1.5e-54;
ive 19; Mismatches 18; Indels
                                                                          le-69;
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Last annotation update)
                                                              DB 1;
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GO; GO: 0008305; C: integrin complex; IEA.
GO; GO: 0007160; P: cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR02035; VWF.A.
Pfam; PF01819; FG-GAP; 3.
Pfam; PF01819; FG-GAP; 3.
PRINTS; PR01818; INTEGRINA.
PRINTS; PR00191; INT.
SMART; SM00191; Int.alpha; 4.
SMART; SM00191; Int.alpha; 4.
SMART; SM00191; VWP, 1.
                      Integrin alpha-M.
                                                            Query Match
100.0%; Score 966; D
Best Local Similarity 99.5%; Pred. No. 1e-6
Matches 188; Conservative 1; Mismatches
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NON TER
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MA-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit.
Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.2%; Score 746; DB 1; Length 1153; Best Local Similarity 77.8%; Pred. No. 7.6e-52; Matches 147; Conservative 20; Mismatches 22; Indels C
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                Cytoplasmic (Potential). FG-GAP 1.
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FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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                            **Springer T. A., Teplow D. B., Derger W.J.;

"Sequence homology of the LFA-1 and Mac-1 leukcoyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukcoyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukcoyte interferon.";

"I glycoproteins and unexpected relation to leukcoyte interferon.";

"I hature 314:340-542(1985).

"I FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles.

"It is identical with (R.-3, the receptor for the third complement component. It probably recognizes the R-G-D peptide in C3D. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAMI. It recognizes Pl and P2 peptides

"I fibrinogen, factor X and ICAMI. It recognizes Pl and P2 peptides

"I fibrinogen, factor X and ICAMI. It recognizes Pl and P2 peptides

"I fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in mast.cell development and in immune complex-mediated

"Glomerulonephritis. Mice expressing a null mutation of the alpha-M sebunit gene demonstrate increase in neutrophil accumulation, in response to a impaired degranulation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocytes.
-!- DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Concains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing; Calcium; Cell adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
Signal; Transmembrane.
SIGNAL 1 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note=No experimental confirmation available; TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                       obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07640; CAA30479.1; -.
EMBL; AK03444; BAC30350.1; -.
EMBL; MAL939; AAA39484.1; -.
EMBL; ML929; AAA39484.1; -.
EMBL; ML939; AAA39484.1; -.
HSSP; P11215; 1BHO.
MGD; MGD; MGD; Ttgam.
GO; GO:000997; C:external side of plasma membrane; IDA.
GO; GO:0001325; P:cell adhesion; IMP.
GO; GO:0045123; P:cellular extravasation; IMP.
GO; GO:0030593; P:neutrophil chemotaxis; IMP.
InterPro; IPR002035; VWF.A.
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Extracellular (Potential).
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SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P05555-2; Sequence=VSP_010473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P05555-1; Sequence=Displayed;
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PROSITE; PS50234; VWFA; 1.
                MEDLINE=85188276; PubMed=3887182;
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PRINTS; PRO0453; VWFADOMAIN.
SWART; SW0191; Int_alpha; 5.
SMART; SM0327; VWA; 1.
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O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.;
"Cloning of rat alpha D, a novel beta 2 integrin.";
"Cloning of rat alpha D, a novel beta 2 integrin.";
"Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
VCAM1. May play a role in the atherosclerotic process such as
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
from the blood (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                              Fathallah D.M. Sr., Zerria K. Jr.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
--- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                  GO; GO:0008305; C:integrin complex; IEA.

R GO; GO:0007160; P:call-matrix adhesion; IEA.

GO:0007229; P:integrin-mediated signaling pathway; IEA.

R InterPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF.A.

R Pfam; PF00183; FG-GAP; 2.

R Pfam; PF00183; VWF.A.

R PRINTS; PR00183; VWFADOMAIN.

R RRINTS; PR00185; VWFADOMAIN.

R SWART; SW00191; Int. alpha; 1.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                Score 719; DB 2; Length 1151;
Pred. No. 1.2e-49;
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(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
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                                                                                                                                                                                                                                                                                                                               74.48;
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Name=Itgad;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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324 IRNQLQEKI 332
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       NCBI_TaxID=10116;
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-i- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-i- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-i- SIMILARITY: Belongs to the integrin alpha chain family.
-i- SIMILARITY: Contains 7 FG-GAP repeats.
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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60.8%; Pred. No. 1.4e-39;
ive 31; Mismatches 43; Indels
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Extracellular (Potential)
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GFFKR motif
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FG-GAP 2.
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FG-GAP
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InterPro; IPR000413; Untegrin_alpha.
InterPro; IPR002015; VWF_A.
Pfam; PF001839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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245 N-111

393 N-111

696 N-111

734 N-111

734 N-111

907 N-111

51045 N-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Signal; Transmembrane SIGNAL 19
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PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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nes 115; Conservative
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    BFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                 121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                              SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE=96257236; PubMed=8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-235 FROM N.A.
SEQUENCE OF 1-235 FROM N.A.
MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9905942; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S., "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96111956; PubMed=8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
"A_novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atheroselerotic process such as clearing lipoproteins from plaques and in phagocytosis of blood-borne pathogens, particulate matter, and senescent erythrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99370002; PubMed=10438935; Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Graygon M.H., Bochner B.S., Gallatin W.M., Staunton D.E.; The leukocyte integrin alpha D beta 2 blinds VCAM-1: evidence for a binding interface between I domain and VCAM-1."; J. Immunol. 163:19984-1990(1999).
                                                                                                                                                                                                                                                             05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2)
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                PRT; 1162 AA.
                                                                                                                                                                                                                      01349; 015575; 015576;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunity 3:683-690(1995).
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH VCAM1.
                                                                                                                               181 IQNQLREKX 189
                                                                                                                                             326 IQRQLQEKI 334
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INTERACTION WITH VCAM1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                   atheroscierotic plaques, and on splenic red pulp macrophages.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
                                            associates with beta-2.

SUBCELULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
lines and subsets of peripheral blood leukocytes and strongly on
tissue-specialized cells, including macrophages foam cells within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell_adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                         SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin alpha-D.
Extracellular (Potential).
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InterPro; IPR002035; VWF.A.

Pfam; PF00357; Integrin_alpha; 1.

Pfam; PF00092; VWA; 1.

PRINTS; PR001185; INTEGRINA.

PRINTS; PR001185; INTEGRINA.

PRINTS; RN00191; Int_alpha; 5.

SWART; SW00191; Int_alpha; 5.
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Potential.
GFFKR motif.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
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FG-GAP 2.
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EMBL; U40279; AAB60638.1; -
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF187881; AAF62875.1; -
HSSP; P11215; IBHQ.
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EMBL, U40274; AAB60534.1; -.
EMBL, U40275; AAB60635.1; -.
EMBL, U40276; AAB60636.1; -.
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**X TRUSUE=100045; PubMed=12477932; DOI=10.1073/pnas.242603899;

**REDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

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**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A postileron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**Robieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Robieton M.J., WcKernan R.J., Malek J.A., Gunaratne P.H.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**Schnerch A., Schein J.E., Jones E.J.M., Marra M.A.,

**Scherztion and initial analysis of more than 15,000 full-length human
                                                                                61 KVVRELPQKINGARDNAAKILVVITDGEKFGDPLNYEDVIPEAEEAGIIRYVIGVXNAFH 120
                                                            KVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFR 149
 MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; "CDNA cloning and complete primary structure of the alpha subunit of laukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                               ITAX HUMAN STANDARD; PRT; 1163 AA.
P20702; QBIVA6;
01-FEB-1991 (Rel. 17, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
01-CCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
11ntegrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CDIIC) (Leu MS).
Name=ITGAX; Synonyms=CDIIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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121 KPQSRRELDTIASKPAGDHVFQVDNFEALNTIRNQLQEKI 160
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Wistar Kyoto;
Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier
Julier C., Masuda J., Yamori Y., Nara Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59801; AAB03226.1; -.
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                                        Potential)
                                                          Potential)
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Pred. No. 7.7e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; GO:0007229; P:integrin-mediated signaling pathway; IEA
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                         43; Indels
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                                                                                                                                                                                                                                                               MW; F296A1A35455D77D CRC64;
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                                                                                                                                                                                       Missing (in Ref. 2).
GHPW -> ATP (in Ref. 2)
L -> V (in Ref. 2).
V -> A (in Ref. 2).
                                                      (GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Pred. No. 1.9e-39;
                                                                                                                                                                     (GlcNAc.
                                        lcNAc
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74.4%;
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PRINTS; PR00453; VWFADOMAIN
SMART; SM00327; VWA; 1.
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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 DSLDYKDVIPWADAAGIIRYAIGVGLAFQNRNSWKELNDIASKPSQEHIFKVEDFDALKD 324
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T-S (in Ref. 4).
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                                                                                                                                                                      209 209 T -> S (in Ref. 4).
251 251 T -> A (in Ref. 4).
490 490 G -> A (in Ref. 4).
547 547 F -> A (in Ref. 4).
556 547 B -> K (in Ref. 4).
556 151 1163 SEK -> TPHYPQDNV (in Ref. 4).
1161 1163 SEK -> TPHYPQDNV (in Ref. 4).
150 157 1 -> V (in Ref. 1).
160 151 1 -> V (in Ref. 1).
161 1163 SEK -> TPHYPQDNV (in Ref. 4).
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                                                                                                                                                                This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                            Integrin alpha-X.
Extracellular (Potential).
Potential.
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FG-GAP 2.
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FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POtential.
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
"Prediction of the Coding Sequences of Mouse Homologues of FJJ Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                          MFLJ00114 protein (Fragment).
Name=mFLJ00114;
Nus musculus (Mouse).
Eukaryots, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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; Pred. No. 1.3e-34;
33; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00242; INTEGRIN ALPHA; UNKNOWN 1.
PROSITE; PS50234; VWFA; 1.
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345 IENQLKEKI 353
                 IQNQLREKX 189
                                                     325 IQNOLKEKI 333
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                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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BAD21383
ID BAD21:
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285 DNLSYDSVIPMAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENPDALKD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 BFONNPNPRSLVKPITOLLGRTHTATGIRKVVRBLFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faculty and the selectively expressed by dendritic cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Integrin alpha-X/Deta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates call-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis (By similarity).
-!-SUBURIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with Deta-2 (By similarity).
-!-SUBCELULAR LOCATION: Type I membrane protein (By similarity).
-!-DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!-SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                         Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene: The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionared Libraries "; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
Name=Itgax;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUR=Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
Tsuchiya H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse),
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                          Mus musculus (Mouse).
Makaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.3%; Score 534; DB 2; 54.5%; Pred. No. 1.3e-34; iive 33; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1169 AA.
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345 IENQLKEKI 353
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103; Conserv
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                                               266 DNLSYDSVIPWAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFDALKD 325
             121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 NFISTSSPLSLLDSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVITDGRKQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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STRAIN=129; TISSUE-Mammary tumor. Brcal-/fl;
Strausberg R.;
Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057200; AAH57200.1; -.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR002035; VWF.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AA; 33404 MW; EC52F3EA48FA068D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                             304 AA.
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                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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nes 80; Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                    181 IQNOLREKX 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                  |:|||:||:
326 IENOLKEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Q6PG66
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO1185; INTEGRINA.
SMART; SMO0191; Int alpha; 5.
SMART; SMO0191; INT alpha; 5.
PROSITE; PSO0243; VWA, 1.
PROSITE; PSS0234; VWFA, 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C616412033C219A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                      MGD; MGI:96609; Itgax.
GO; GO:0009897; C:external side of plasma membrane; IDA InterPro; IPR000413; Integrin_alpha.
InterPro; IPR02035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin alpha-X.
Extracellular (Potential)
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FG-GAP 1.
FG-GAP 2.
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SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
GFFKR motif
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Potential.
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FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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Pfam, PF00357; Integrin_alpha, 1.
Pfam, PF00092; VWA; 1.
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                                                                                                                                                                                                                                                                                          EMBL; AF211864; AAF23492.1; -.
HSSP; P20702; 1N3Y.
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SMART; SM00191; Int_alpha; 4
SMART; SM00327; VWA; 1.
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PRINTS; PR00453; VWFADOMAIN
      Itgae protein (Fragment).
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Pfam; PF00092; VWA; 1.
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358 LLSKLQQRI 366
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AF133074;
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AF133078;
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AF133081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF133076;
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O88340;
01-NOV-1998 (
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STRAIN:129; TISSUE=Mammary tumor. Brcal-/fl;

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bark N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max G.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rapleton M., Soarse M.B., Bonaldo M.F., Carannor P., Frange C.,

RA Brownstein M.J., Usdin T.B., Tooshlyuki S., Carannor P., Frange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKwan P.J., McKernan K.J., Maake J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Sodergren E.J., Lu X., Glbbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Sodiigues S., Sanchez A.,

Rhiting M., Madan A., Young A., Green E.D., Dickson M.C.

Rhotiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Romerselion and initial analysis of more than 15,000 full-length human merchan
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7,
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STRAIN-129; TISSUE-Mammary tumor. Brcal-/fl;
Straubberg R.;
Stubmitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                          02-WAR-2004 (TrEMBLrel. 27, Last sequence update) 02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
266 DNLSYDSVIPMAEAASIIRYAIGVGHKDGF 295
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                                                                                                                                                                                          304 AA
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(TrEMBLrel. 12, L
(TrEMBLrel. 24, L
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Mus musculus (Mouse).
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01-NOV-1999
01-JUN-2003
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178 EDGTEIAIVLDGSGSIEPSDFQKAKNFISTMMRNFYEKCFECNFALVQYGAVIQTEFDLQ 237
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10095;
                                                                                                                                                                                      Schoen M.P., Arya A., Murphy E.A., Adams C.M., Strauch U.G.,
Agace W.W., Marsal J., Donohue J.P., Her H., Beier D.R., Olson S.,
Lefrancols L., Brenner M.B., Grusby M.J., Parker C.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;
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(TrEMBLrel. 08, Last sequence update)
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GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
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Cell adhesion; Integrin; Transmembrane.
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AAD30063.1; JOINED.
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InterPro, IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF133085; AA330063.1; -. EMBL, AF133070; AAD30063.1; JOINED. RMBL, AF133071; AAD30063.1; JOINED.
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AAD30063.1; JOINED.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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61 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                         311 DPINLTTVINSPKMOGVVRFAIGVGDAFKNNNTYRELKLIASDPKEAHTFKVTNYSALDG 370
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                                        Integrin alpha El.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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371 LLSKLQQRI 379
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Search completed: January 13, 2005, 15:18:43 Job time : 40.5668 secs

alp bet alp bet

Mouse

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integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant; osteopathic; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thromboals; cancer; osteoporoals; sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
                                                          Rat alpha
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Abab67374
Aaw62107
Aaw73348
Aaw73348
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Aar771
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Aar8167
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ABG61486
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AAW65102
AAW53835
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AAW65104
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17-JUL-2002; 2002US-0396790P.
11-SEP-2002; 2002US-0410135P.
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Maximum DB
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Database

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subunits where one of the subunits has one or more mutations, an altered surface feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-oysteine residue to cysteine or extracellular domains of integrin alpha and beta subunits. The polypoptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic cytostatic, immunospresses, antifilamatory, neuroprotective and antisickling activities and may be useful for immunotherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple sclerosis. The current sequence is that of the human integrin alpham subunit precursor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                  144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                          263
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                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
Rosenberg S;
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                                                                                                                                                                                                                                                               Length 1152;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                            100.0%; Score 966; DB 8; 99.5%; Pred. No. 2.5e-96; iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by mRNA of the invention #45.
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20-DEC-2002; 2002US-00325899.
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                               Sequence 1152 AA;
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Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of

genes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                    The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The method are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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non-specific defence system; integrin gene superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha subunit of Mac-1 leukocyte adhesion receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 966; DB 8; 99.5%; Pred. No. 2.5e-96; iive 1; Mismatches 0
Claim 65; SEQ ID NO 2444; 1762pp; English.
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/label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1152 AA;
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This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
                   EFONNPNPRSLVKPITOLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening assay for modulators of integrin binding - using immobilised o:
labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis.
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Pred. No. 2.5e-96;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Beta-integrin CD11b subunit protein.
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                                                                                                                                                                                                                                                                                        AAW65090 standard; protein; 1153 AA
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99.5%; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)
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Label= putative N-glycosylation site
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89US-00321239
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Matches 188; Conservative
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N-PSDB; AAQ04043.
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09-MAR-1989;
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit alpha d (AnAboul and AnBo71s9). The present sequence has approximately 60% identity to the protein sequence of alpha d. The Alpha_d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple sclerosis, aethma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies can also be used to detect and system injury. The monoclonal antibodies can also be used to detect and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system
   DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                            264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; macrophage infiltration inhibition, alpha d integrin;
leukocyte integrin; Leu-CAM; leukointegrin; immune response;
inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
lung inflammation; acute respiratory distress syndrome; Crohn's disease;
rheumatoid arthritis; central nervous system injury; CD11b.
                                                                                                                                                                                                                                                                                                                                                                                       AAB07360 standard; protein; 1153 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CD11b protein sequence.
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diagnose Crohn's disease
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                                                                                                                                        IQNQLREKX 189
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Length 1153;

100.0%; Score 966; DB 3; 99.5%; Pred. No. 2.5e-96;

Query Match Best Local Similarity

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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immunosuppressive activities. The polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain, and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-IFA-I antibody) is useful for tratering or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the
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                                                                                                                                                           DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified integrin-I or integrin I-like domain polypeptide useful as an immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired
                                                                                                               EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                              1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.
Gaps
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0; Indels
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human integrin 1 alpha-M subunit protein.
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binding of an integrin to a cognate ligand such as Crohn's disease, nephritis; human immunodeficiency virus (HIV), myocardial infarction, slorgen's syndrome; rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human polypeptides of the invention
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Example 5; Page 191-194; 270pp; English

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The invention relates to promoting locomotor recovery, inhibiting autonomic and sensory dysfunction following spinal cord injury by administering autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-Ro v VCAM-I (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft, atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative collitis, immune complex alveolities and leukaemia. The present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the
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The invention comprises structurally biased variant integrin inserted (I) domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins. The integrin I domain proteins and nucleic acids encoding the variant integrin I domain proteins or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatoid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating: ischaemia/ repertusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer The variant integrin I domain nucleic acids and infection and sense therapy, as vaccines and to screen for bloactive agents. The present amino acid sequence represents the Mac-1 alpha subunit of integrin
                                                                                                                                                   New integrin I domain protein having alteration in at least 2 noncontiguous regions and exits in an open conformation, useful for treating, preventing or suppressing inflammatory or immunological
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Sequence 1153 AA;

144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203 263 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVANFEALKT 180 323 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120 9 EFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK DPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT Gaps ö Score 966; DB 5; Length 1153; Pred. No. 2.5e-96; 0; Indels Pred. No. 2.5e 1; Mismatches 100.0%; 99.5%; P Matches 188; Conservative IQNQLREKX 189 324 IQNOLREKI 332 Local Similarity 204 121 264 181 61 Query Match g ò g ò g ð

ADD25615 standard; protein; 1153 AA. ADD25615;

Binding domain-immunoglobulin fusion protein-associated protein #85. (first entry) 15-JAN-2004

Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease. 

Unidentified

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The invention relates to a binding domain-immunoglobulin tusion process.

Comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide. The constant region polypeptide comprises: a wild-type human igdi immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutetach human igdi immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human igdi immunoglobulin hinge region polypeptide contains 2 costeine residues; where the first cysteine is not mutated; a mutated human igdi immunoglobulin hinge region polypeptide contains on more than one cysteine residues; where the mutated human igdi immunoglobulin hinge region polypeptide contains no cysteine residue; and a mutated human igdi immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains cospable of at least one immunological activity comprising the contains of capable of at least one immunoglobulin hinge region polypeptide contains construct comprising the polymuclectide (operably linked to a promoter), a recombinant expression construct comprising the polymuclectide (operably linked to a promoter).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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US2003118592-A1.
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVWEQLKKSKTLFSLMQYSEEFRIHFTFK 203 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEFFRIHFTFK 60 ;; 0 0; Indels 100.0%; Score 966; DB 7; 99.5%; Pred. No. 2.5e-96; ive 1; Mismatches 0 Matches 188; Conservative Query Match Best Local Similarity

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Sequence 1153 AA;

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The invention relates to a Factor B analogue that exhibits modified complement activity in vitro. The analogue is generated by substituting a bort compensus repeat domain (SCR) or a von Willebrand Factor domain (SCR) or a will willebrand Factor domain (WWP) of human factor B with a SCR or a wWF from a second protein such as human complement activity complement involved in immune and autoimmune responses. Complement activity can account for substantial tissue damage in a wide variety of autoimmune complex mediated syndromes auch as lupus erythematosus, can account for substantial tissue damage in a wide variety of autoimmune complement system using the analogues is likely to provide a means of the complement system using the analogues. Is likely to provide a means of the rapeutic intervention in these cases. Inhibition of complement may also be favorable in cases that involve tissue damage caused by vascular injury such as myocardial infarction, creebral vascular accidents or acute shock lung syndrome. In these cases the complement system may contribute to the destruction of partially damaged tissue as in reperfusion injury. In addition, the use of complement system may contribute to the destruction of partially damaged tissue as in the prevention of xenograft rejection (the inhibition is important in the prevention of xenograft rejection (the inhibition of complement by cell-associated and soluble inhibitors is useful in protecting the transplant from damage caused by activation of endogenous complement. The present sequence represents the vWF domain of human factor MAC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Factor B analogue; modified; complement activity; complement factor B; short consensus repeat domain; von Willebrand Factor domain; human; C2; CR3; autoimmune response; tissue damage; lupus erythematosus; therapy; rheumatoid arthritis; hemolytic anemia; myasthemia gravis; injury; MAC-1; myocardial infarction; acute shock lung syndrome; inflammation; vWF.
BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                          263
                                                                                      DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                   323
                       204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                                                                264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding complement protein homologues useful for modulating function of the complement system in the treatment of variety of immune and autoimmune complex mediated syndromes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human complement factor MAC-1 vWF domain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5A-B; 53pp; English.
                                                                                                                                                                                                                                                                                                                                     AAY21991 standard; protein; 187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00687706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00177109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIW ) UNIV WASHINGTON
                                                                                                                                                                             IONOLREKX 189
                                                                                                                                                                                                                     324 IQNQLREKI 332
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                                                                                                                                                                                                                                                                                                                                                                                  AAY21991;
61
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AAY21991
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                                                                                                                                                                          EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                               121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-11ke domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Gly, Ala
/note= "Wild-type Ile substituted by Gly or Ala"
                                                                     .
0
                                         Length 187;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human integrin alpha subunit CD11b variant A domain.
                                                                    0
                                                      8.9e-97;
                                      DB 2;
                                                100.0%; Prec. ...
                                         Score 960;
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                                                                                                                                                                                                                                                                                                                                                                     AAU76856 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2000; 2000US-021950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2001; 2001WO-US023957
                                         99.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                  Matches 187; Conservative
                                                                                                                                                                                                                                                                      IONOLRE 187
                                                                                                                                                                                                                                                                                               181 IONOLRE 187
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                                                        Similarity
              Sequence 187 AA;
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Synthetic.
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WPI; 2002-188687/24

CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or seridue 315 and A at residue 320 have been replaced by C, is useful C or determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds or to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemiater reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847 

Sequence 191 AA;

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120
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                                                                 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                              121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT
                                                                                                EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT
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0
Score 956; DB 5; Length 191;
Pred. No. 2.5e-96;
                        2; Mismatches
 99.0%;
                        Matches 186; Conservative
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                                                                                                                                                                                                   IQNQLREKX 189
             Local Similarity
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AAU76847 standard; protein; 191 AA (first entry) 21-MAY-2002 AAU76847; RESULT 12 AAU76847

Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-11ke domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy. Human integrin alpha subunit CD11b A domain.

 188
 note= "This region is specifically claimed" Location/Qualifiers Region

31-JUL-2001; 2001WO-US023957

WO200209737-A1 Homo sapiens. X EX X B X B B X C

07-FEB-2002

31-JUL-2000; 2000US-0221950P 11-JAN-2001; 2001US-00758493 13-MAR-2001; 2001US-00805354. (GEHO ) GEN HOSPITAL CORP.

Arnaout AM, Li R, Xiong J;

The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 313 and A at residue 320 have been replaced by C, or CD1b or contracting if a test compound is a candidate compound for binding for determining if a test compound is a candidate compound for binding to the polypeptide and determining if the test compound binds to the polypeptide and determining if the test compound binds skeletal muscle injury, for treating disorders caused by ischaemia-representing injury, increating disorders caused by ischaemia-reperfusion injury, increating disorders caused by ischaemia-reperfusion injury, increating disorders and parasitic diseases, to purify variant integrin polypeptide 11qands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain. integrin alpha subunit CD11b A domain Sxample 2, Fig 5, 55pp; English. Sequence 191 AA; 

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                                                                                                            9
                                                                                                                                                                       61 BFQNNFNPRSLVKPITQLLGRTHIATGIRKVVRELFNITNGARKNAFKLLVVLTDGEKFG
                                                                                                                                                                                                                                            1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                   61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                          1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                       Gaps
                                       :
0
Query Match 99.0%; Score 956; DB 5; Length 191; Best Local Similarity 97.9%; Pred. No. 2.5e-96; Matches 185; Conservative 3; Mismatches 1; Indels
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AAB66766

181 İQNQLREKI 189

AAB66766 standard; protein; 216 AA. (first entry) 10-APR-2001 AAB66766;

EST; expressed sequence tag; inclusion body; binding partner; immunoglobulins. Amino acids 149-353 of human CR-3 alpha chain and His tag. WO200102588-A2 Homo sapiens. Synthetic 

(MORP-) MORPHOSYS AG.

30-JUN-2000; 2000WO-EP006137.

99EP-00112815

12-JUL-1999;

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Misc-difference 172
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          WO9529243-A1
                                                  19-APR-1995;
                                                                      26-APR-1994;
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AAU76866
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                                      Generating specific binding partners to (poly)peptides encoded by genomic DNA fragments, involves forming inclusion bodies by expressing the (poly)peptide as part of fusion proteins.
                                                                                                                                                                                                                                                                                                  PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGY 125
                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                                                                           EDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQVNNFEALKTIGNQL 185
                                                                                                                                                                                                                                                                                                                                                       132 EDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Spacer
/note= "spacer allows accommodation of Factor-Xa at the
cleavage site"
                                                                                                                                                                                                                                                                                                             PNPRSLVKPITQLIGRTHTATGIRKVVRELFNITNGARKOAFKILVVITDGEKFGDFLGY
                                                                                                                                                                                                                                                           SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                                                        SDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte beta-2-integrin Mac-1; I-domain; CD11b; fusion protein; glutathione-S-transferase; GST; Factor-Xa; antiinflammatory.
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                  96.7%; Score 934; DB 4; Length 216; 99.5%; Pred. No. 7.8e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222. .228
/label= Factor-Xa_recognition_sequence
 Von Rueden T;
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Hoess A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR77461 standard; peptide; 435 AA.
                                                                                Disclosure; Page 18; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231. .435
/label= I-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GST-I-domain fusion protein.
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/label= GST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
 Kretzschmar T,
                                                                                                                                                                                                                                      Matches 183; Conservative
                   WPI; 2001-147085/15.
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   REKX 189
                                                                                                                                                                                                                                                                                                                                                                                                       REKI 195
                                                                                                                                                                                               Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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12-FEB-1996
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 Frisch C,
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Protein
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A fusion protein comprises a glutathione-S-transferase fusion partner, used to increase the level of soluble protein expression in B. coli and to facilitate affinity purification, and the human leukocyte beta-1 integrin Mac-1 I-domain, linked by a Factor-Xa recognition sequence that allows cleavage of the fusion protein and recovery of the I-domain, which is useful as an antiinflammatory. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                       Glutathione-S-transferase fusion protein with Factor Xa cleavage site for prodn. of I-domain from leukocyte B2-integrin Mac-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 EDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 2.1e-93;
1; Mismatches 0; Indels
                                                                                                                                                                                       Fairbanks MB
                                                                                                                                                                                       Tomich CC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 32-34; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU76866 standard; protein; 177 AA
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95WO-US004439.
                                                       94US-00233596
                                                                                                                                                                                       Anderson DC,
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                                                                                                                                                                                                                                                                                   WPI; 1995-382991/49
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                                                                                                                                                                                                                        Bajt-Jaeschke ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 435 AA;
                                                                                                                         (UPJO ) UPJOHN
                                                                                                                                                                                       Heinrikson RL,
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 332 has been replaced by C CD11b alpha subunit A domain, where I at residue 332 has been replaced by C OT V at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful to for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing to the polypeptide. The integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b deletion variant A domain. Note: This cariant sequence is not featured in the specification but has been compared to the protein shown in AAU76847
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
/note= "Wild-type Val substituted by Cys"
                                        /note= "Wild-type Ala substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page; 55pp; English
                                                                                                                                                                          31-JUL-2001; 2001WO-US023957.
                                                                                                                                                                                                                 31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                                                                                                                                                                                                                                                                                                                  Arnaout AM, Li R, Xiong J;
                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-188687/24
                    Misc-difference 177
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                                                                                    WO200209737-A1
                                                                                                                               07-FEB-2002
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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVWEQLKKSKTLFSLMQYSEEFRIHFTFK 60 61 BFQNNPNPRSLVKPITQLLGRTHIATGIRKVVRELFNITNGARKNAFKLLVVLTDGEKFG 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 61 ò 8 8 셤

120

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Gaps 0,

Query Match
92.4%; Score 893; DB 5; Length 177;
Best Local Similarity 97.7%; Pred. No. 1.9e-89;
Matches 172; Conservative 2; Mismatches 2; Indels

DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 176 DPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNPE 176 121 121

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Search completed: January 13, 2005, 15:12:32 Job time : 36.3364 secs

Scoring table:

Searched:

Database

Sequence:

Run on:

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Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; Publication No. US20030078375A1
; Publication No. US20030078375A1
; GENERAL INFORMATION;
; APPLICANT: Arnacy Jana-ping
; APPLICANT: Li, Rui
; APPLICANT: Li, Rui
; APPLICANT: Kiong, Jian-ping
; TITLE OP INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/758,493
; RIOR APPLICATION NUMBER: US 60/221,950
; RRIOR APPLICATION NUMBER: US 60/221,950
; RRIOR APPLICATION NUMBER: US 60/221,950
; RRIOR PILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE FEASTSEQ for Windows Version 4.0
; SEQ ID NO 1
: LENGTH: 191
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Sequence 3, Appl
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6 US-10-615-515-9

5 US-10-346-863-17

6 US-10-346-863-48

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0 US-10-346-863-48

0 US-09-795-872-5

0 US-09-902-4814-3

1 US-09-902-4814-3

1 US-09-891-943-37

0 US-09-891-943-55

0 US-09-891-943-101

0 US-09-891-943-101

0 US-09-891-943-46

0 US-09-805-359-3

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0 US-09-801-943-7
    ; TYPE: PRT
; ORGANISM: Homo sapiens
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Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 37, Appli
                                                                                                    January 13, 2005, 15:13:36; Search time 31.2304 Seconds (without alignments) 2186.449 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.ppp:*
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| Cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.ppp:*
| Cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.ppp:*
                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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1 US-09-758-493-1

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US-09-945-265-4

US-09-912-813-1

US-09-912-41A-1

US-09-912-41A-1

US-10-144-259-30

US-10-144-259-30

US-10-207-655-176

US-09-902-481A-6

US-09-902-481A-6

US-09-902-481A-6

US-09-902-481A-6

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US-09-902-481A-6

US-10-346-863-37
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           1608061 seqs, 361289386 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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966
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Maximum DB seq length: 200000000
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                              Copyright
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Match
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Perfect score:
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Score

Result No.

966 9966 9966 9966 9967 749 9951 9951

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Best Local Similarity 99.5
Matches 188; Conservative
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181 IQNQLREKI 189
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ORGANISM: Homo sapiens
TYPE: PRT ORGANISM: Homo sapiens
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                                   US-10-144-259-1
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Publication No US20030109691A1
| GENERAL INPORMATION:
| APPLICANT: Arraout, M. Amin
| APPLICANT: Li, Rui
| APPLICANT: Li, Rui
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| APPLICANT: Li, Rui
| FILE REFERENCE: 10786-548001
| CURRENT APPLICATION NUMBER: US/10/144,259
| CURRENT FILING DATE: 200-09-04
| PRIOR FILING DATE: 2000-10-11
| PRIOR FILING DATE: 2000-07-31
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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100.0%; Score 966; DB 11; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                       Sequence 1, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
    APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui -Ping
    TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
    TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 191
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ORGANISM: Homo sapiens
US-09-758-493-1
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US-09-758-493-1
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LENGTH: 191

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61 EFONNPNPRSLVKPITOLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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Query Match 100.0%; Score 966; DB 14; Length 191; Best Local Similarity 99.5%; Pred. No. 1.6e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0;
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US-09-350-259-3
'Sequence 3, Application US/09350259
'Patent No. US20020062008A1
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Query Match 100.0%; Score 966; DB 10; Length 1153; Best Local Similarity 99.5%; Pred. No. 1.9e-92; Matches 188; Conservative 1; Mismatches 0; Indels 0;
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; Publication No US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT FILING DATE: 1998-11-16-26
; PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
; PRIOR FILING DATE: 1994-08-05
; PRIOR FILING DATE: 1994-12-1
; PRIOR FILING DATE: 1994-12-1
; PRIOR FILING DATE: 1994-12-1
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
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ORGANISM: Homo sapiens
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Publication No. US20030054440A1

GENERAL INFORMATION:

APPLICANT: Springer, Timothy

APPLICANT: Shifman, Julia

APPLICANT: Shifman, Julia

APPLICANT: Mayo, Stephen

TITLE OF INVENTION: NUMBER: US/09/902, 481A

CURRENT FILING DATE: 2001-07-07

PRIOR PAPLICATION NUMBER: US 60/216,600

PRIOR PLILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1.
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100.0%; Score 966; DB 9;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0;
               APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
ATTLE OF INVENTION: No. US20020062008Alel Human 2
FILE REFERENCE: 27866/35004
                                                                                                           CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
EARLIER FILING DATE: 1994-10-03
EARLIER FILING DATE: 1994-10-03
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CORGANISM: Homo sapiens
US-09-350-259-3
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ORGANISM: Homo sapiens
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NAME/KEY: mat_peptide
LOCATION: (17)..()
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US-09-902-481A-1
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US-09-902-481A-1
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264 DPLGYEDVIPBADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFFALKT 323
                                                                                                                                                                                                                                                      ; Sequence 6, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION:
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Best Local Similarity 97.4%;
Matches 184; Conservative
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                                      APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
CHILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-07-31
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: LIS3
TYPE: PRI CHING DATE: 2000-07-31
NUMBER: PSEQ FOr Windows Version 4.0
SEQ ID NO 30
LENGTH: 1153
TYPE: PRI PRIOR Sapiens
US-10-144-259-30
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Sequence 176, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNCGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT PILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOUTHARE: Patentin version 3.0
SEQ ID NO 176
LENGTH: 1153
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Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0;
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US-10-207-655-176
                       GENERAL INFORMATION:
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APPLICANT: Springer, Timothy
APPLICANT: Springer, Moccomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2000-07-09
PRIOR PILIOR DATE: 2000-07-07
PRIOR PILIOR DATE: 2000-07-07
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-615-515-9
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CRGANISM: Homo sapiens
US-10-346-863-37
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| JENERAL INCREMITED |
| APPLICANT: Shimmoka, Motomu |
| APPLICANT: Shimmon, Julia |
| APPLICANT: Shimmon, Julia |
| APPLICANT: Mayo, Stephen |
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY |
| FILE REFERENCE: A-70586-1/RPT/RNS/RMK |
| CURRENT APPLICATION NUMBER: US 60/216,600 |
| PRIOR PILING DATE: 2001-07-09 |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 4 |
| LENGTH: 1137
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                                                                                                           Query Match 98.4%; Score 951; DB 10; Length 1137; Best Local Similarity 95.2%; Pred. No. 7.1e-91; Matches 180; Conservative 8; Mismatches 1; Indels 0
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TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
                                   FEATURE:
CTHER INFORMATION: synthetic
US-09-902-481A-5
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65 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
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APPLICANT: FAGAN, RICHARD, JOSEPH; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN; APPLICANT: GUTTERIOGE, ALEX; TITLE OF INVENTION: ADHESION MOLECULES; FILE REFRENCE: 674575-2004; CURRENT FILING DATE: 2003-07-08; CURRENT FILING DATE: 2003-01-11; PRIOR APPLICATION NUMBER: GB 0100750.9; PRIOR FILING DATE: 2001-01-11; NUMBER OF SEQ ID NOS: 12; SEQ ID NO 9; SEQ ID NO 9; LENGTH: 187
Sequence 37, Application US/10346863
Publication No US20040038325A1
GENERAL INPORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: PAGAN, RICHARD JOSEPH
APPLICANT: GUTTERINGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT APPLICATION NUMBER: PCT/GB01/03318
PRIOR PILING DATE: 2003-01-17
PRIOR PILING DATE: 2001-07-24
PRIOR PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
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Best Local Similarity
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NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
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                                              5 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFKEFQN
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Best Local Similarity 100.0%; Pred. No. 1.1e-90;
Matches 184; Conservative 0; Mismatches 0; Indels
0; Indels
1; Mismatches
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FUDLication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: PRGAN, RICHARD JOSEPH
APPLICANT: GUTTERIDGE, ALEX
ITILE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB0/103318
PRIOR PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PLING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-10-17
SOFTWARE: PALICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-10-17
SOFTWARE: PALICATION NUMBER: GB 0025447.4
FRIOR FILING DATE: 2000-10-17
SOFTWARE: PALENTING DATE: 2000-10-17
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Job time : 32.2304 secs
Matches 184; Conservative
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; ORGANISM: Homo sapiens
US-10-346-863-17
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LREKI 185
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APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUREY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/637,830
FILING DATE: 21-MAR-1991
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,830
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/539,830
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: 07/539,830
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US-08-193-043-55
US-09-183-043-55
US-09-180-255-55
US-09-350-256-55
US-08-485-618-101
US-08-943-363-101
US-08-943-363-101
US-08-193-043-101
US-08-193-043-101
US-09-183-043-101
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US-08-183-048-101
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Patent No. 5877275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REPERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 8EQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
        TYPE: amino acid
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STATE: MA
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     Sequence 43, Appl
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                             version 5.1.6
- 2005 Compugen Ltd.
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PCT-US96-01314-43
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US-09-350-259-37
US-08-485-618-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                             GenCore (c) 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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No.
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204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                               121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     5424322--
; PACENT: ARNAOUT, M. AMIN
; TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
; UNIMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/78,871
; FILING DATE: 16-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 539,842
; FILING DATE: 18-JUN-1996
; APPLICATION NUMBER: 212,573
; FILING DATE: 28-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-173-497-3
; Sequence 3, Application US/08173497
; Patent No. 5437958
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Best Local Similarity 99.5
Matches 188; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 233 S.
CITY: Chicago
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STATE: I1
COUNTRY:
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                                                                                                               61 BFQNNPNPRSLVKPITQLLGRIHTAIGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                            121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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  Length 1152;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: M. AMIN ARIAOUT
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCES: 78
CORRESPONDENCES: FACHARDON P.C.
STREET: 225 Franklin Street
100.0%; Score 966; DB 2; 99.5%; Pred. No. 5.2e-93;
                    Pred. No. 5.2e
1; Mismatches
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COUNTEX: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
NAME: JOHN W. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Version 5.0)
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TELECOMMUNICATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-8906
                    Best Local Similarity 99.5
Matches 188; Conservative
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INFORMATION FOR SEQ ID NO:
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324 IQNQLREKI 332
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Matches 188; Conser
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PCT-US96-01314-43
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Query Match
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61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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STATE: 111inois
COUNTRY: United States
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC compatible
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REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                             TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
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Patent No. 5470953
GENERAL INFORMATION,
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INFUNITION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 966; DB 1; Length 1153; 99.5%; Pred. No. 5.2e-93; tive 1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/173,497
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
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CITY: Chicago
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US-08-286-889-3
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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                                                                                                                                                                                                     ; Score 966; DB 1; Length 1153; Pred. No. 5.2e-93; 1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA: GRAPHICATION DATA: PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                     100.0%;
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                                     1153 amino acids
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  Matches 188; Conservative
            SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino aci
                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-362-652-3
                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 IQNQLREKI 332
                                                      TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                           Local Similarity
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US-08-605-672-3
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Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                               Score 966; DB 1; Length 1153; red. No. 5.2e-93;
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
                                                                                                                                                                                                                                                                                                                        Pred. No. 5.2e
1; Mismatches
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659,659,673290
TELEPRAN: 312-474-6300
TELERA: 312-474-0448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 188; Conservative 1
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TELEFAX: 312-474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INFORMINS: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bornn
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                                                                                                                                                                                     Query Match 100.0%; Score 966; DB 2; Length 1153; Best Local Similarity 99.5%; Pred. No. 5.2e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0.
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233 South Wacker Drive, 6300 Sear Tower
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COMPUTER READ-8402
COMPUTER FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
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; TYPE: amino acid
; STRANDENNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 IQNOLREKX 189
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US-08-482-293A-3

Sequence 3, Application US/08482293A

PAtent No. 2831029

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Monica

TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                     Query Match 100.0%; Score 966; DB 2; Length 1153; Best Local Similarity 99.5%; Pred. No. 5.2e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0;
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233 South Wacker Drive, 6300 Sear Tower
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CONTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
PILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 27866
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 3:
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      1153 amino acids
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                       TYPE: amino acid
STRANDEDNESS: single
FOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3
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RESULT 12
US-09-688-307A-3
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                                                                                                         ; Score 966; DB 2; Length 1153; Pred. No. 5.2e-93; 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQUENCE 3. Application US/09193043
Fatent No. 6551395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TILE CO INVENTION:
FILE REPERBNCE: 27866/35004
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 08/193,043
CURRENT FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
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EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
                                                                                                       Query Match
Best Local Similarity 99.5%; 1
Matches 188; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 1153

TYPE: PRT

CORGANISM: Homo sapiens

US-09-193-043-3
                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-943-363-3
STRANDEDNESS: single
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                                                                                                                                         61 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                        1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSBEFRIHFTFK
    0; Gaps
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    0, Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26-JUL-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: S14
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%; Score 960; DB 2;
100.0%; Pred. No. 2e-93;
iive 0; Mismatches 0
    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 61, Application US/08687706
Patent No. 5928892
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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amino acid
    Matches 187; Conservative
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Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                           181 IQNQLRE 187
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US-08-687-706-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPLGYEDVI PEADREGVI RYVI GVGDAFRSEKSRQELNTI ASKPPRDHVFQVNNFEALKT 323
                                                                                                                                                                                                                                                                                                     1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                       0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
SPOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-7AN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pablet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/08177109A
Patent No. 5869615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby: TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       Query Match 100.0%; Score 966; DB 4; Best Local Similarity 99.5%; Pred. No. 5.2e-93; Matches 188; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (404) 873-8794
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 187 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQNOLREKX 189
                                                                                                              TYPE: PRT
CORGANISM: Homo mapiens
US-09-350-259-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-177-109A-61
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                                                                                         LENGTH: 1153
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Mon Feb 28 05:50:43 2005
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121 DPLGYEDVIPEADREGVIRYVIGYGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
181 IQNQLRE 187
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181 IQNQLRE 187
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Search completed: January 13, 2005, 15:34:34 Job time : 10.0829 secs

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5.1.6
Compugen Ltd.
version -
GenCore (c) 1993
        Copyright
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- protein search, using sw model OM protein January 13, 2005, 15:03:32 ; Search time 5.12706 Seconds (without alignments) 3321.665 Million cell updates/sec Run on:

RWHU1B-C\_COPY\_144\_320

922 1 CPQEDSDIAFLIDGSGSIIP......NTIASKPPRDHVFQCNNFEC'177 Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	cell surface qlyco	ocyte su	cell surface glyco	integrin alpha-E c	cell surface glyco	ឃី	cartilage matrix p	cartilage matrix p	matrix	al prot	alph	alpha 1	alpha 1		integrin alpha-1 c		integrin alpha-1 -	integrin alpha-1 c		collagen alpha 1(V	alpha 2			collagen alpha 3 (V		hypothetical prote	2	immunodominant mic	von Willebrand fac
SUMMAKIES	OI	RWHU1B	S00551	RWHU1C	A53213	803308	156126	A33809	S66522	A37979	S42373	A45974	S31212	S78476	A40020	A45226	T46488	A55348	A35854	151027	A54849	I45914	A37797	A33998	CGHU3A	S44142	T23760	S32604	A45638	UMHU
	DB	-	~	~	~	~	~	~	N	N	N	~	N	7	~	7	N	N	7	~	7	7	0	~	N	7	7	0	0	Н
	Length	1153	1153	1163	1179	1170	1163	493	200	496	3051	1747	1857	1888	3124	1151	741	272	1180	929	2944	1170	3137	1181	3176	1178	550	371	712	2813
ф	Query Match	97.9	75.1	52.7	33.5	28.8	56.6	24.6	24.1	23.3	21.3	21.1	21.1	21.1	20.8	20.5	19.5	19.1	18.6	17.8	17.1	16.4	16.3	15.6	15.6	15.3	15.0	14.8	14.6	14.3
	Score	903	692	486	309	265.5	245	227	222	215	196.5		194.5	194.5	an.		179.5	176.5	171.5	164	157.5	151	150.5	144	144	141	138	136	•	132
	Result No.	-	7	Ю	4	ß	9	7	80	O	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

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A40970	150807	S04111	147230	S21369	A48569	C35243	S09646	CGHU2A	S23377	A32856	G00039	PS0323	T28797	T16580	S34839
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843 2	763 2	1022 2	191 2	1029 1	724 2	238 2	917 2	1018 1	918 2	1019 1	427 2	414 2	567 2	13055 2	1025 2
.9 843 2										*				_	
13.9 843 2	13.8 763 2									*				_	
13.9		13.5	13.2	13.1	13.0	13.0	13.0	13.0	12.9	12.7	12.5	12.3	11.9	11.8	11.5

## ALIGNMENTS

-1	
3	ΞB

Nighternate glycoprotein CD11b precursor [validated] - human
Nighternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Maceusocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004
Cipacession: A31.08; A28915; A41600; A30892; A32218; A46526; A26091; I52567
Cipate: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004
Cipacession: A31.08; A28915; A11601; A30892; A32218; A46526; A26091; I52567
J. Biol. Chem. 263, 12403-12411, 1988
Airtle: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)

A; Reference number: A31108; MUID:88315033; PMID:2457584

A, Accession: A31108
A, Molecule type: mRNA
A, Residuas: 1-1153 < COR>
A, Residuas: 1-1153 < COR>
A, Residuas: 1-1153 < COR>
A, Residuas: 1-1153 < COR>
A, Rosa-references: UNIPROT: P11215; GB: J03925; NID: g187284; PIDN: AAA59544.1; PID: g307148
A; Note: part of this sequence was confirmed by protein sequencing
R, Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
C, Cell Biol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor McA; Reference number: A28915; MUD: 88257215; PMID: 2454931

A; Accession: A28915

A; Molecule type: mRNA
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confirm R; Shelley, C.S.; Arnaout, M.A.
B; Shelley, C.S.; Arnaout, M.A.
Broc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg.
A; Reference number: A41600; MUID:92073318; PMID:1683702

A; Molecule type: DNA A; Residues: 1-9 <SHE>

A;Cross-references: GB:W76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R;Arnaout, M.A.; Remold-O'Donnell, B.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85; 2776-2780, 1988
A;Title: Wolecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic A;Reference number: A94193; WUID:88190151; PMID:2833753

A; Accession: A30892

A;Molecule type: mRNA A;Residues: 917-1042 <AR2>

A,Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Rrickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A.F.C. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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R;Corbi, A.L.; Garcia-Aguilar, J.; Sp.
J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
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Best Local Similarity 77.39
Matches 136; Conservative
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A; Residues: 1-834 < CO2>
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A; Map position: 16p11.2-16p11.2
A; Note: promoter contains a GATA motif and two Sp1 consensus binding sites
A; Note: promoter contains a GATA motif and two Willebrand factor type A repeat home
C; Superfamally: cell surface glycoprotein CD1b; von Willebrand factor type A repeat home
C; Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C; Keywords: alternative splicing; calcium; predicted <SIG>
F; 1-16 / Domain: signal sequence #status predicted <SIG>
F; 1-110 / Domain: signal sequence glycoprotein CD1b #status experimental <MAT>
F; 17-1108 / Domain: extracellular #status predicted <AXY>
F; 17-1108 / Domain: calcium/magnesium binding #status predicted
F; 530-538 / Region: calcium/magnesium binding #status predicted
F; 530-601 / Region: calcium/magnesium binding #status predicted
F; 1109-1134 / Domain: intracellular #status predicted <INM>
F; 1108-1153 / Domain: intracellular #status predicted <INNT>
F; 113-1153 / Domain: intracellular #status predicted <INT>
F; 113-1154 / Domain: intracellular #status predicted <INT>
F; 115-1154 / Domain: intracellular #status predicted <INT>
F; 115-1154 / Domain: intracellular #status predicted <INT>
F; 115-1154 / Domain: intracellular #status predicted <INT>
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F; 115-1154 / Domain: intracellular #status predicted <INT>
F; 115-1154 / Domain: intracellular #status predicted <INT>
F; 115-1154 / Domain: intracellular #status 
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A; Residues: 1-499,501-1153 <FLE>
A; Cross-references: GB: S52227; NID: g263047; PIDN: AAB24821.1; PID: g263049
A; Note: the last three bases of intron 13, CAG, are included in some but not all mature A; Note: sequence extracted from NCBI backbone (NCBIP: 121963)
A; Note: sequence extracted from NCBI backbone (NCBIP: 121963)
B; Pierree, M.W.; Remold-O'Donnelly, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A; Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp. A; Reference number: A90664; MUID: 87076671; PMID: 3539202
                                                                                                                                gene and phylogenetic analysis of the alpha-in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: IS2567
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Crossidues: 1-9 <RES>
A;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
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Note: part of this sequence was confirmed by protein sequencing ?leming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G. Immunol. 150, 480-490, 1993
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R; Pall, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A; Title: Characterization of the myeloid-specific CD11b promoter.
A; Reference number: I52567; MUID:92144986; PMID:1346576
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Pred. No. 5.6e-72;
0; Mismatches 1; Indels
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                                                                                                                                A, Title: Structural analysis of the CD11b n during evolution.
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C;Comment: A common bet:
C;Genetics:
A;Gene: GDB:ITGAM; CR3A
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AjGene: Mac-1

(S.Superfamily: cell surface glycoprotein; transmembrane protein

C;Superfamily: cell adhesion; glycoprotein; transmembrane protein

C;Keywords: cell adhesion; glycoprotein (SIG)

F;1-16/Domain: signal sequence #status predicted (SIG)

F;1-15/Product: leukcoyte surface glycoprotein Mac-1 alpha chain #status experimental

F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>

F;1106-1129/Domain: transmembrane #status predicted <TWM>
EMBO J. 7, 1371-1378, 1988
A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
A;Reference number: S00551; MUID:88312584; PMID:3044779
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R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
Embo J. 6, 4023-4028, 1987
A;Title: CDNA cloning and complete primary structure of the alpha subunit of a leukocyte A;Reference number: S00864; WUID:88166645; PMID:3327687
A;Accession: S00864
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1153 <-PYT>
A; Residues: 1-1153 <-PYT>
A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983;
A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983;
A; Note: the authors translated the codon CAC for residue 569 as Gln
R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A; Reference number: 159078; MUID:86287312; PMID:2942940
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AjAccession: A36584

AjAccessiudes: 1-1163 «COR»

AjCross-references: UNIPROT:P20702

AjCross-references: UNIPROT:P20702

AjCross-references: UNIPROT:P20702

AjCorbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.

J. Biol. Chem. 265, 2782-2788, 1990

AjTitle: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.

AjAccession: A35543; MUID:90153906; PMID:2303426
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NiAlternate names: leukocyte adhesion receptor p150,95 alpha chain
CiSpecies: Homo sapiens (man)
Cibace: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
CiAccesion: A36584; A35543; S00864
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A;Cross references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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fuction-associated molecule-1-alpha - mouse
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A;Cross-references: GDB:119757; OMIM:153370
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Matches 58; Conservative
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A; Residues: 1-20 < COR>
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Residues: 1-20 <SHE>
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A;Residues: 1-20 <NUE>
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
F;199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
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A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:700093; NID:9487829; PIDN:AAA59180.1; PID:9487830
A;Octos-references: GB:M81695; EMBL:700093; NID:9487829; PIDN:AAA59180.1; PID:9487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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A; Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. A; Reference number: A53213; MUID:94164962; PMID:8119947
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TEIAIILDGSGSIDPPDFQRAKDFISNWARNFYEKCFECNFALVQYGGVIQTEFDLRDSQ 260
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C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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A,Stetus: prellminary
A;Molecule type: mRNA
A;Residues: 1-1179 <SHA>
A;Cross_references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245
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38.4%; Pred. No. 3.2e-19;
iive 39; Mismatches 65;
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Best Local Similarity
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Cell Burface glycoprotein CD11a precursor - human N;Alernate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: S03308; A47458; A47555; A48759; S36044 R;Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T. J. Cell Biol. 108, 703-712, 1989 A;Tille: Primary structure of the leukocyte function-associated molecule-1 alpha subunit: A;Reference number: S03308; MUD:89139587; PMID:2537322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A;Title: Identification of cell-specific and developmentally regulated nuclear factors t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: part of this sequence was confirmed by protein sequencing
R;Cornwell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A;Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pron
A;Reference number: A47458; MUID:93248261; PMID:8097887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: Y00796; NID: 931421; PIDN: CAA6874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 DYVKWKDPDALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGE--A 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 TDSGNIDAAKD----IRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GB:M95609
R;Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Balol. Cham. 268, 19305-19311, 1993
A;Title: Charcrization of the CD1a (alphal, LFA-talpha)
A;Reference number: A48759; WUID:93374910; PMID:8103515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: A47565; MUID:93281759; PMID:8099450
Accession: A47565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.8%; Score 265.5; DB 2; 33.0%; Pred. No. 2.3e-15; ive 44; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-1170 <LAR>
A;Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8;
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C;Species: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shc J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix I A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage matrix protein precursor - mouse C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S6652
R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Bur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein ct
A;Reference number: S66522; MUID:96270751; PMID:8665920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A reper F;1-29/Domain: signal sequence #status predicted <SIG> F;30-500/Product: cartilage matrix protein #status predicted <MAT> F;31-500/Pomain: von Willebrand factor type A repeat homology <VWA1> F;231-266/Domain: EGF homology <EGF> F;237-441/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 157-290, L', 292-496 «JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT: P51942; EMBL: U35035; NID: g1163178; PIDN: AAB06521.1; PID: g116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                           65 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 NNPNPRSLVKPITQLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --QDYINDAARKAKDLGFKMFAVGVGNAV----EEELREIASEPVADHYFYTADFK 442
                                                                                          6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTL--FSLMQYSEEFRIHFTFKEFQ
                                                                                                                                                                                                                                            | | : | : | : | : | | : | | 386 -QDYITDAAKKAKDLGFRMFAVGVGNAV----EDELREIASEPVAEHYFYTADF
                                                                                                                                                                                             125 YEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941; GB:J05667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein precursor - human
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Best Local Similarity 30.5%
Matches 54; Conservative
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                                                               Rikaufmann, Y.; Teeng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit a
A;Reference number: IS6126, MUID:91268576; PMID:2051027
A;Accession: I56126
A;Accession: Is6126
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Cartilage matrix protein precursor - chicken

C;Species allus gallus (chicken)

C;Species allus gallus (chicken)

C;Date: 09-Mar-1990 #Beaquence_revision 09-Mar-1990 #text_change 09-Jul-2004

C;Accession: A33809; A26364

E;Kiss, I: Deak, F: Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argr B:Acl. Chem. 264, 8126-8134, 1989

A;Title: Structure of the gene for cartilage matrix protein, a modular protein of the exgrins, You Willebrand factor, complement factors B and C2, and epidermal growth factor.

A;Reference number: A33809; MUID:89255246; PMID:2542265
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A; Residues: 1-493 <KIS>
A; Residues: 1-493 <KIS>
A; Cross-references: UNIPROT: P05099; GB: X12346; GB: X12347; GB: X12348; GB: X12349; GB: X1235
R; Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A; Title: Structural features of cartilage matrix protein deduced from cDNA.
A; Reference number: A26364; MUID: 87092429; PMID: 3025875
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A;Residues: 78-493 cARG>
A;Cresidues: 78-493 cARG>
A;Creserreferences: GB:MI4792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F;37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : |: || || || || || CMKGKVDLVFLFDGSQSLDRKDFBEKILBFWKDVMRKLSNTSYQFAAVQFSTDCRTEFTFL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS--KTLFSLMQYSEEFRIHFTFKEFQN 64
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156126
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F;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 245; DB 2; Length 1163;
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.6%; Score 245; DB ilarity 32.6%; Pred. No. 1.5e Conservative 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 60; Conserv
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Best Local Similarity
Matches 56; Conserv
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A; Molecule type: mRNA
A; Redecidues: 286-494, O', 496-834, A', 836-1119, KL', 1122-1402,1409-1439 <TRU>
A; Regordon, M. X.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F
Bur. J. Biochem. 201, 333-338, 1991
A; Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens v
A; Reference number: 817035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Molecule type: protein
A/Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A/Rolecule type: protein
A/Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C/Resynords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes
C/Resynords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes
C/Resynords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes
C/Resynords: alternative splicing; coiled coil.
C/Resynords: fibronectin type III repeat homology <RN3D>
C/Resynords: fibronectin type III repeat homology <RN3D>
C/Resynords: fibronectin type III repeat homology <RN3D>
C/Resynords: fibronectin type III repeat homology <RN3C>
C/Resynords: fibronectin type III repeat homology <RN3C>
C/Resynords: fibronectin type III repeat homology <RN3C>
C/Resynords: von Willebrand factor type A repeat homology
C/Resynords: von Willebrand factor type A repeat homology
C/Resynords: non-collagenous NC2 #status predicted <NC3>
C/Resynords: riple helical domain COLI #status predicted <COLI>
COLI>
COLI #status predicted <COLI>
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J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920 CKAAKADLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTBF 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1040 SQDD---VNKVSREMQLDGFSFFAIGVADADYS----ELVNIGSKPSERHVFFVDDFD 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFV-STV--MEQLKKSKTLFSLMQYSEEFRIHF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 KFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
S31212
collagen alpha 1(XIV) chain precursor, short form - chicken
C,Species: Gallus gallus (chicken)
C,Species: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                          A;Residues: 1-1747 <CER.>
A;Cross-references: UNIPROT: P32018
A;Cross-references: UNIPROT: P32018
A;Cross-references: UNIPROT: P32018
A;Experimental source: embryo skin with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83; Indels 11; Gaps
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                                                                                                               A; Reference number: A45974; MUID: 93280195; PMID: 8505337
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Best Local Similarity 31.8%; Pred. No. 7.6e-09;
Matches 57; Conservative 28; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EWBL Data Library, March 1992 A;Reference number: $30085 A;Accession: $30085
                                                                                                                                                       A, Accession: A45974
A, Status: preliminary
A, Molecule type: mRNA; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1472-1659 <GOR1>
Accession: S20833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1472-1660 <APT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: S17035
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N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952/2; 1041/1; 1146/1;
                                                                       C;Superfamily: cartilage matrix protein; BGF homology; von Willebrand factor type A repe
C;Keywords: glycoprotein; homorrimer
C;Keywords: glycoprotein; homorrimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-496/Product: cartilage matrix protein #status predicted <WAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 HFTFKEFQNNPNPRSLVKPITQ---LLGRTHTATGIRKVVRELFNITNGAR---KNAFKI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPKQKTDLVPLIDGSGSIGSYVPKNEVLRFVREFVE--LFEIGRSKTRVGLIQYSDQIRH 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 EFDLDQYGDRD---SLLKGISETQYLTGLTRTGAAIQHWVQEGFSERRGARPQQSDIARV 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T20G5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C;Accession: S42373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 LVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTL--FSLMQYSEEFRIHFTFKEFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPQEDSDIAFLIDGSGSIIPHDF-----RRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRI
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                                                                                                                                                                                                                                                              F;27-262/Domain: EGF homology <EGF> F;77-262/Domain: Willebrand factor type A repeat homology <VWA2> F;76.344/Binding site: carbohydrate (Asn) (Covalent) #status predicted F;221-238,234-247,249-262/Disulfide bonds: #status predicted
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F;512-679/Domain: von Willebrand factor type A repeat homology <VWAl>
F;754-799/Domain: fibronectin type II repeat homology <VRI>
F;154-194/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 215; DB 2; Length 496; 29.9%; Pred. No. 2.5e-11; tive 38; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Indels
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A;Residues: 1-3051 <SMI>A;Residues: 1-3051 <SMI>A;Coss-references: EMBL:Z30423; NID:g458479; PID:g458485
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%;
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nes 57; Conservative
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A;Rolegues: 1-1857 «WAE>
A;Rosserterences: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
C;Genetics:
C;Genetics:
A;Gene: Col14A1
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-1857/Product: fibronectin type III repeat homology <FN3S>
F;352-433/Domain: fibronectin type III repeat homology <FN3S>
F;534-614/Domain: fibronectin type III repeat homology <FN3E>
F;74-633/Domain: fibronectin type III repeat homology <FN3E>
F;74-633/Domain: fibronectin type III repeat homology <FN3E>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-1009/Domain: fibronectin type III repeat homology <FN3G>
F;822-1009/Domain: fibronectin type III repeat homology <FN3G>
F;822-1009/Domain: fibronectin type III repeat homology <FN3G>
F;812-1009/Domain: 
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A,Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:92888
A,Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:92888
EMBL: J. Biochem. 212, 483-490, 1993
A,Title: Complete primary structure of chicken collagen XIV.
A,Reference number: S31211; MUID:93185668; PMID:8444186
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1-28/Domain: signal sequence #status predicted <81G>
1-29-188/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
1-29-110/Domain: fibronectin type III repeat homology <FN3A>
1-166-320/Domain: von Willebrand factor type A repeat homology <VWAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1096 KLMAYKTKETLLEAIQQIAYKGGNTKTGKAİKHAREVLFTGEAGMRKGIPKVLVVITDGR 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQDD---VNKVSREMQLDGFSFFAIGVADADYS-----ELVNIGSKPSERHVFFVDDFD 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPQEDSDIAFLIDGSGSIIPHDFRRMKEFV-STV--MEQLKKSKTLFSLMQYSEEFRIHF
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                                                     B.; Winterhalter, K.H.; Trueb,
                                                                                                                                                                                                                                                              Status: nucleic acid sequence not shown; translation not shown
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C;Accession: S31212
R;Waaclchi, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
R;Waaclchi, C.; Trueb, 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31212
A;Accession: G31212
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Pred. No. 8.2e-09
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A;Cross-references: EMBL:X70793
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31.8%;
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R; Trueb, B.
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C, Genetics:
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22\overline{25}54; S28811
G;Accession: A40020; A34485; B34485, A.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obare J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule winous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Reference number: A40020; MUID:92011862; PMID:1918137
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A; Residues: 2772-2792;2846-2873 < GOR2>
B; Gordon, M.K.; Gerecke, D.R.; Olben, B.R.
B; Gordon, M.K.; Gerecke, U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix component discovered by CDNA cl
A; Reference number: A28037; MUD:87317590; PMID:3476925
A; Recession: A28037
A; Reference number: A28037; MUD:87317590; PMID:3476925
A; Residues: 2960-2976, F', 2978-3074, 'AG' < GOR3>
A; Residues: 2960-2976, F', 2978-3074, 'AG' < GOR3>
A; Residues: BMBL:M17375; NID:9211649; PIDN:AAA48718.1; PID:9211650
A; Reference has been revised in reference A34485
B; Koch, M.; Bernasconi, C.; Chiquet, M.
Bur. J. Biochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of the A; Reference number: S23814; MUID:9236621; PMID:1323460
A; Reference number: S23814
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A;Molecule type: mRNA
A;Residues: 1-3124 «YAMA
A;Residues: 1-3124 «YAMA
A;Cross-references: UNIPROT: P13944; GB:D00824; NID:G222810; PIDN:BAA00701.1; PID:G222811
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
B;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type IN
A;Reference number: A34485; MUID:90062079; PMID:2584192
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A;Residues: 'X',1333'(0',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 <}
A;Residues: 'X',1333'(0',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 <}
R;Dublet, B.; van der Rest, M.
A; Biol. Chem. 262, 17724-1777, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-c
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A;Molecule type: mRNA
A;Residues: 2456-2758, A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1888;
F;352-433/Domain: fibronectin type III repeat homology <FN3B> 4742-255/Domain: fibronectin type III repeat homology <FN3C> F;534-614/Domain: fibronectin type III repeat homology <FN3D> F;623-707/Domain: fibronectin type III repeat homology <FN3D> F;741-823/Domain: fibronectin type III repeat homology <FN3E> F;741-823/Domain: fibronectin type III repeat homology <FN3F> F;922-1009/Domain: fibronectin type III repeat homology <FN3F> F;922-1009/Domain: fibronectin type III repeat homology <FN3G> F;1040-1205/Domain: won Willebrand factor type A repeat homology
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Thirrons: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1

Thirrons: 2845/3; 2863/3; 2810 cell binding; coiled coil; connective tissue; disulfid interpretation is signal sequence #status predicted <21G.

The status product: collagen alpha 1(XII) chain short splice form #status predicted /24-1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted /24-114/Domain: IIIA #status predicted <1IIA.

The status predicted <1IIA.

The status predicted <1IIA.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.

The status predicted <1IIB.
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1630-71178/Domain: fibronectin type III repeat homology <FN3C>
1721-802/Domain: fibronectin type III repeat homology <FN3D>
1812-895/Domain: fibronectin type III repeat homology <FN3E>
1805-986/Domain: fibronectin type III repeat homology <FN3F>
1805-986/Domain: fibronectin type III repeat homology <FN3F>
1908-1076/Domain: fibronectin type III repeat homology <FN3H>
1197-1361/Domain: von Willebrand factor type A repeat homology <
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                                                                                                                       Trueb, J.; Trueb, B.
Cochim. Biophys. Acta 1171, 97-98, 1992
Title: The two splice variants of collagen XII share a'common 5'
Reference number: 828811; MUID:93042014; PMID:1420368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 192; DB 2; Length 3124; ; Pred. No. 2.6e-08; 34; Mismatches 72; Indels 18
                                                                                                                                                                                                                                                                                                    Molecule Lype: mRNA
Residues: 1-24,1189-1257,'8',1259-1263,'E',1265-1280 <TRU>
Crose-references: BMBL:X67327
                                                        Molecule type: protein
Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
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ibronectin type III repeat homology
A; Reference number: $22254; MUID:88087065; PMID:3121603
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RESULT 15

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A45226
R;Briesswitz, R.; Epstein, M.R.; Marcantonio, B.E.
J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
A;Accession: A45226
A;Status: preliminary; not compared with conceptual translation
A;Accession: A45226
A;Status: preliminary; not compared with conceptual translation
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-1151 - BRIS
A;Cross-references: UNIPROT: P56199
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itegrin alpha-1 chain - human (fragment)
Species: Homo sapiens (man)
Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

Corbi A.L., Kishimoto J.K., Miller L.J., Springer T.A.;

"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, you Willebrand factor and factor B.";

J. Biol. Chem. 263:12403-12411(1988).
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MEDLINE=88190151; PubMed=2833753;
Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
Arnaout Cloning of the alpha subunit of human and guinea pig
1eukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLINE=88257215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
Cell Biol. 106:2153-2158(1988).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
11-0CT-2014 (Rel. 45, Last annotation update)
01-0CT-2014 (Rel. 45, Last annotation update)
11-0CT-2014 (Rel. 45, Last annotation u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "CDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
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MEDLINE-89098893; PubMed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
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PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
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GO; GO:0007125; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin alpha.
InterPro; IPR002035; WWF_A.
Pfam; PP01839; FG-GAP; 3.
Pfam; PP00092; INTEGRIN alpha; 1.
Pfam; PP00092; WWA; 1.
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EMBL, J04145; AAA59491.1; --
EMBL, S52127; AAA59903.1; --
EMBL, S52127; AAA54821.1; --
EMBL, S52152; AAA24821.1; JOINE
EMBL, S52153; AAA24821.1; JOINE
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PDB; 1BHO; X-ray; 1/2=-
PDB; 1BHO; X-ray; 1/2=-
PDB; 1DN; X-ray; 0=140-331.
PDB; 1UDN; X-ray; 0=143-331.
PDB; 1UM; X-ray; 0=143-331.
PDB; 1MIV; X-ray; 0=143-337.
PDB; 1MY; X-ray; A=144-337.
PDB; 1MS2; X-ray; A=140-335.
PDB; 1NA5; X-ray; A=140-335.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
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MEDLINE-98226734; PubMed-9560195;

A Oxvig C., Springer T.A.;

Be units and a calcium binding site on its lower surface.";

subunits and a calcium binding site on its lower surface.";

subunits and a calcium binding site on its lower surface.";

reconstructions of monocytes, macrophages and granulocytes adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAMI. It recognizes Pl and P2 peptides of fibrinogen gamma chain.

C. ISUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M associates with beta-2.

C. ISUBCELLULAR LOCATION: Type I membrane protein.

C. INESTITE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOWAIN: The integrin I-domain (insert) is a VWPA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains I WWPA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl1b.htm".
                                                                                                                                                                                                                                                                                                                                             SECUENCE OF 17-31.
MEDLINE=87076671; PubMed=3539202;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
W.-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa.";
Biochim. Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95171458; PubMed-7867070; Liddington R.; Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE-96363671; PubMed-8747460;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
                                   SEQUENCE OF 1-9 FROM N.A.
MEDLINE-92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                                                                                                       MEDLINE=92144986; PubMed=1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
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  Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 3:1333-1340(1995).
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Structure 6:923-935(1998).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                 Score 903; DB 1; Length 1152;
Pred. No. 7.4e-67;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
            Integrin alpha-M.
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PRINTS; PRO0423; VWFADOWAIN.
SWART; SMO0191; Int_alpha; 4.
SWART; SMO0327; VWA; 1.
PROSITE; PSS0224; VWFR; 1.
Cell adhesion; Integrin; Transmembrane.
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as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M.beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes Pl and P2 peptides of fibrinogen gamma chain. Alpha-M.beta-2 play a critical role in mast call development and in immune complex-mediated glomerulonephritis. Mice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophil accumulation, in response to a impaired degranulation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop
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PROSITE; PS50234; VNPA; 1.
Alernative splicing, Call adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                          Isold=P05555-2; Sequence=VSP_010473;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                        EMBL; X07640; CAA30479.1; -.

EMBL; AX039444; BAC30350.1; -.

EMBL; MA4293; AAA39484.1; -.

EMBL; MA4293; AAA39484.1; -.

EMBL; S1215; 18055.1

HSSP; P11215; 18055.1

AGO; GO:0007155; P:cell adhesion; IMP.

GO; GO:0007155; P:cell adhesion; IMP.

GO; GO:0045123; P:cell adhesion; IMP.

GO; GO:0045123; P:cell adhesion; IMP.

GO; GO:0046123; P:cell adhesion; IMP.

AGO; GO:004613; P:cell adhesion; IMP.

AGO; GO:004613; Integrin_alpha.

Efam; PF00035; VWF_A.

R Pfam; PF00095; VWF, A.

R Pfam; PF00095; VWF, A.

R Pfam; PR00055; Integrin_alpha; 1.

R PRINTS; PR0185; INTEGRINA.

R SMRRT; SM00191; Int alpha; 5.

SMART; SM00191; Int alpha; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin alpha-M.
Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential) FG-GAP 1.
                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                              IsoId=P05555-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
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SIGNAL 1
CHAIN 17 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
1106
1130
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85
164
337
401
                                                                                                                                                                                                                                                                 Name=1;
                                                                                                                                                                                                                                                                                               Name=2;
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fathallah D.M. Sr., Zerria K. Jr., Sathallah D.M. Sr., Zerria K. Jr., Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
-- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL, AF268593; AAF81280.1; --
HNSSP; PIL155; HBHQ.
GO, 60:0008105; C:integrin complex; IEA.
GO, GO:0008105; P:cell-matrix adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
(Potential)
(Potential)
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(Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127480 MW; 178DB988AECB0343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in isoform
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V -> G (in Ref. 2)
                                                                                                               By similarity.
By similarity.
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Potential.
GFFKR motif.
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FG-GAP 6.
FG-GAP 7.
                                   Potential
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683
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1153 AA;
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PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                      Integrin alpha-D.
Extracellular (Potential)
                                                                                                                                                                                                                                                                Potential.
Cytoplasmic (Potential)
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Potential
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
                                          InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; VWF_A.
InterPro; IPR02035; VWF_A.
Pfam; PF01819; FG-GAP; 3.
Pfam; PF00187; Integrin_alpha; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
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FG-GAP 2.
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SIGNAL 1 19
                   EMBL; AF021334; AAF21241.1;
HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 106; Conservative
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ID TIAD HUMAN STANDARD,
AC Q13349; Q15575; Q15576;
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1100
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602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallatin W.M.;

"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, beta-2 is a receptor for ICAM3 and volumed (MQC-1997) to the EMBL/GenBank/DobU databases.

"CAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloddborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similatity).

"SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

"SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

"SUBUNIT: Hoterodimer of an alpha and a very domain. Integrins with 1-domains do not undergo procease cleavage.

"Integrin Belongs to the integrin alpha chain family.

"SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                              61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
                                                                                                                                                                                                                                                                                                                                                                       DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                     ö
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF A.

Pfam; PF01839; FG-GAP; 2.

R Pfam; PF001839; FG-GAP; 2.

R Pfam; PF00185; Integrin_alpha; 1.

R PRINTS; PR00191; Int_alpha; 5.

R SMART; SM00191; Int_alpha; 5.

R SMART; SM00191; Int_alpha; 5.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.

R PROSITE; PS0224; VWFA; 1.

R PROSITE; PS0224; VWFA; 1.

R PROSITE; PS0224; VWFA; 1.

R PROSITE; PS0224; VWFA; 1.

R PROSITE; PS0224; VWFA; 1.
                                                                                                                                                                                                      Score 669; DB 2; Length 1151;
Pred. No. 3e-47;
11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
                                                                                                                                                                                               72.64; Sco. No. 3e. 73.94; Prod. No. 3e. 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1161 AA
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Name=Itgad;
                                                                                                                                                                                                                                  Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNF 175
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                   59.7%; Score 550; DB 1; Length 1161; 60.6%; Pred. No. 2.8e-37; tive 27; Mismatches 42; Indels (
                                                                                                                                                                                                 1161 AA; 126600 MW; 2258491A984A705E CRC64;
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J. Exp. Med. 188:2187-2191(1998).
                          MEDLINE=96111956; PubMed=8777714;
                                      Immunity 3:683-690(1995).
                                                                          INTERACTION WITH VCAM1.
                                                                                               INTERACTION WITH VCAM1.
                      SEQUENCE FROM N.A.
                        TISSUE=Spleen;
        Name=ITGAD
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MIM; 602453; --

CO; GO:0008305; C:integrin complex; TAS.

GO; GO:0016337; P:cell-adria adhesion; NAS.

GO; GO:001637; P:cell-matrix adhesion; NAS.

GO; GO:001635; P:immune response; NAS.

GO; GO:000413; Integrin_alpha.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR000413; Integrin_alpha.

Ream; PF00357; Integrin_alpha; 1.

Ream; PF00357; Integrin_alpha; 1.

Ream; PF00357; Integrin_alpha; 1.

Ream; PF00357; Integrin_alpha; 1.

Ream; PF00357; Integrin_alpha; 1.

Ream; PR00185; Integrin_alpha; 1.

Ream; PR00185; Integrin_alpha; 5.

Ream; Ream; Ream; Ream; Integrin Alpha; 1.

Repeat; SS00242; INTEGRIN ALPHA; 1.

Repeat; SS00242; INTEGRIN ALPHA; 1.

Repeat; Signal; Transmembrane.

Repeat; Signal; Pransmembrane.

Transmembrane.

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or send an email to license@isb-sib.ch)
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EMBL, U40277, AAB60636.1; --
EMBL, U40277, AAB60637.1; --
EMBL, U40279, AAB60638.1; --
EMBL, U40279, AAB60638.1; --
EMBL, T40278, AAB60638.1; --
EMBL, P11215, IBHQ.
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MEDLINE-99370002; PubMed=10438935;

A van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,

RA van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,

RA drayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;

The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a strong interface between I domain and VCAM-1:";

Li Immunol. 163:1984-1990(1999).

C I Immunol. 163:1984-1990(1999).

C I Immunol. 163:1984-1990(1999).

C I EWNTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes clamper pathogens, particulate matter, and senescent erythrocytes in the blood.

C I SUBMNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2.

C I SUBCIELULAR LOCATION: Type I membrane protein.

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Lines and subsets of peripheral blood leukocytes and strongly on tissue-specialized cells, including macrophages.

C I SUBCIELULAR LOCATION: Type I membrane protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-235 FROM N.A. MEDLINE-20187620; PubMed=10722744; Noti 'D., Johnson A.K., Dillon J.D., Structural and functional characterization of the leukocyte integrin "Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Sp1 and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
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Staunton D.E., Gallatin W.M.;
"A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2)
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Gaps

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-CCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu MS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F., Julier C., Masuda J., Yamori Y., Nara Y.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U59801; AAB03226.1; -- GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.1e-36;
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01-FEB-1991 (Rel. 17, Created)
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74.1%;
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MEDINES-218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINES-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Joanes M.B., Moore T., Wax S.L., Wang J., Heish F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Redriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield M.S., John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J. John J
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-1- SIMILARITY: Belongs to the integrin alpha chain family.
-1- SIMILARITY: Contains 7 FG-GAP repeats.
-1- SIMILARITY: Contains 1 VWFA domain.
-1- DATABASE: NAME-ERGW; NOTE-CD guide CD11c entry;
-1- DATABASE: NAME-ERGW; NOTE-CD guide CD11c entry;
-1- WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially
                                                                                                                                              of
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MEDLINE-88166645; PubMed-3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
Corbi A.L., Miller b.J., O'Connor K., Larson R.S., Springer T.A.;
Corbi A.L., Miller b.J., O'Connor K., Larson R.S., Springer T.A.;
Inch Miller adhesion glycoprotesion, pls0,95.";
EMBO J. 6:4023-4028(1987).
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SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
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J. Biol. Chem. 265:12750-12751(1990).
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J. Immunol. 138:2381-2383(1987).
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61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kikuno R., Ohara O., Koga H.;

Baga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;

"Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:

The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous CDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
111 — TaxID=10090,
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  D -> L (in Ref. 1).
I -> V (in Ref. 4).
SEK -> TPHYPQDNV (in Ref. 4).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
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    1163 AA;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GFFKR motif.

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N-linked (GlCNAc. .) (Potential).
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T - S (in Ref. 4).
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G -> A (in Ref. 2).
E -> K (in Ref. 2).
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VWFA.
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                                                        EMBL; M29165; -; NOT ANNOTATED CDS. EMBL; M29165; -; NOT ANNOTATED CDS. EMBL; M29487; AAA5.670.1; ALT SEQ. EMBL; M29482; AAA5.620.1; JOINED. EMBL; M29483; AAA5.620.1; JOINED. EMBL; M29484; AAA5.620.1; JOINED. EMBL; M29486; AAA5.620.1; JOINED. EMBL; M29486; AAA5.620.1; JOINED. EMBL; BC038237; AAA5.620.1; JOINED. EMBL; BC038237; AAA5.620.1; JOINED.
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Potential
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SIGNAL 1
                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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C. -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

REMBL, AKI31131, BAD21383.1, -.

REMBL, AKI31131, BAD21383.1, -.

R GO: GO: 0009897; C: external gide of plasma membrane; IDA.

R InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR002035; VWF_A.

R Pfam; PF01839; RG-GAP; 3.

R Pfam; PF00357; Integrin_alpha; 1.

R Pfam; PF00357; Integrin_alpha; 1.

R Pfam; PR00357; Integrin_alpha; 1.

R RINTS; RR0185; INTEGRINA.

R RINTS; RR0185; INTEGRINA.

R RINTS; RR01911; Inte alpha; 5.

R SWART; SM00227; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; "Prediction of the Coding Sequences of Mouse Homologues of FlJ Gene: The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                               285 DNLSYDSVIPMAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFD 340
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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; Pred. No. 1.2e-31;
30; Mismatches 53; Indels (
                                                                                                                                                                                                                                                      52.4%; Score 483; DB 2; Length 1188; 52.8%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                              53; Indels
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                      PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
PROSITE; PS50234; VWPA; 1.
Cell adhesion; Integrin; Transmembrane.
                                                                                                                                                                                                                                                                              30; Mismatches
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Submitted (DEC-1999) to the EMBL/GenBank/DBM databases.

Submitted (DEC-1999) to the EMBL/GenBank/DBM databases.

Insolation of genes selectively expressed by dendritic cells.";

Submitted (DEC-1999) to the EMBL/GenBank/DBM databases.

Interaction interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis (By similarity).

SUBMIT: Heterodimer of an alpha and beta submit. Alpha-X associates with beta-2 (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

SUBMIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Contains 7 FG-GAP repeats.
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285 DNLSYDSVIPWARAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD110).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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GG); GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR003235; VWF A.
Pfam; PF01839; RG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
PRINTS; PR00453; VWA; 1.
PRINTS; PR00453; VWAPADAMAIN.
SMART; SM00191; Int_alpha; 5.
SWART; SM00127; VWA; 1.
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Integrin alpha-X.
Extracellular (Potential).
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Integrin alpha X.
Mus musculus (Mouse)
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SEQUENCE
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MEDINE-22388257; PubMed=12477932,

MEDINE-22388257; PubMed=12477932,

MACHAINE-22388257; PubMed=12477932,

MACHAINER R.D., Colling F.S., Wagner L.H., Derge J.G., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MACHAINER R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MACHAINER R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MACHAINER R.F., Jordan H., Moore T., Machain C.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Parage C.,

MARA B.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MACHAINER S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MACHAIN S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MALIALON D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan A., Youchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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1169 AA; 129150 MW;
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nes 93; Conservative
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STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 NFISTSSPLSLLDSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLJVITDGRKQG 265
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=129, TISSUE-Mammary tumor. Brcal-/fl;
Strausberg R.;
Submiled (Aug. 2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC057200, AAH57200.1; -.
GO; GO:0007229, P:integrin-mediated signaling pathway; IEA.
InterPro; IPR002035; VWF.A.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
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PROSITE; PS50234; VWPA; 1.
Cell adhesion; Integrin; Transmembrane.
NON_TER 1 1 1
NON_TER 895 895
SEQÜENCE 895 AA; 98265 MW; BE6EA14A
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                                                                                                                                                              Query Match
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Q8BS01;
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Matches
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Agace W.W., Marsal J., Donohue J.P., Her H., Beier D.R., Olson S.,
Lefrancois L., Brenner M.B., Grusby M.J., Parker C.M.;
Lefrancois L., Brenner M.B., Grusby M.J., Parker C.M.;
Submitted (WAR-1999) to the EMBL/Genbank/DDBJ databases.
-!-SUBCELULAR LOCATION: Type I membrane protein (By similarity).
EMBL; AR133079; AAD30063.1; JOINED.
BRBL; AR133077; AAD30063.1; JOINED.
BRBL; AR133077; AAD30063.1; JOINED.
BRBL; AR133077; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133078; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
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BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133081; AAD30063.1; JOINED.
BRBL; AR133084; AAD30063.1; JOINED.
BRBL; AR133084; AAD30063.1; JOINED.
BRBL; AR133084; AAD30063.1; JOINED.
BRBL; AR133084; AAD30063.1; JOINED.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                   44.3%; Score 408; DB 2; Length 304; 53.3%; Pred. No. 5.1e-26; Wative 25; Mismatches 43; Indels
[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS7200; AAH57200.1; -.
                                                                                                                                                                                   304 AA; 33404 MW; EC52F3EA48FA068D CRC64;
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Last annotation update)
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PRINTS; PR00453; VWFADOMAIN
SMART; SM00191; Int. alpha; 4
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                         80; Conservative
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Name=Itgae;
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                                                                                                                                                                                   SEQUENCE
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178 EDGTEIAIVLDGSGSIEPSDFQKAKNFISTWARNFYEKCFECNFALVQYGAVIQTEFDLQ 237
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STRANTE-STBL/G1 TISSUE-Aorta and vein;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/G0; TISSUE=Aorta and vein;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 DPLNLTTVINSPKMQGVVRFAIGVGDAFKNNNTYRELKLIASDPKEAHTFKVTNY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530055J10 product:integrin, alpha E,
epithelial-associated, full insert sequence.
                                                                       Length 895;
                                                                                                                                           66, Indels
895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;
                                                               34.9%; Score 322; DB 2; 38.3%; Pred. No. 2.7e-18; iive 40; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Aorta and vein; MBDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1038 AA
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=20530913; PubMed=11076861;
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=21085660; Pubmed=11217851;
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 Carninci P.
         Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Samamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RTKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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MGD; MGI:1298377; Itgae.

GO; GO:00001160; P:call-matrix adhesion; IEA.

GO; GO:0007126; P:integrin-mediated signaling pathway; IEA.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR02035; VWF.A.

Pfam; PF01839; PG4P; 3.

Pfam; PF01839; WA; 1.
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Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1038 AA; 114722 MW; 2EBIDE7660795587 CRC64;
Sasaki N.,
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 Itoh M., Aizawa K.,
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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                                                                                                                             SEQUENCE FROM N.A.
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Search completed: January 13, 2005, 15:18:44 Job time : 38.0546 secs

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AAW65101 AAW72834 AAW73344 AAR07371	ABG61480 AAR781480 AAR73062 AAW60004	AAW55104 AAW72824 AAB07345 AAB07374 ABG61483	AAR 8179 AAR 78166 AAW 23049 AAW 23064 AAW 57491 AAW 55106 AAW 55089
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## ALIGNMENTS

Homo sapiens. Synthetic. H Key Location/Qualifiers
T Misc-difference 172
T Mote= "Wild-type Val substituted by Cys"

WO200209737-A1.

07-FEB-2002.

31-JUL-2001; 2001WO-US023957.

31-JUL-2000; 2000US-0221950P. 11-JAN-2001; 2001US-00758493. 13-MAR-2001; 2001US-00805354.

(GEHO ) GEN HOSPITAL CORP.

Arnaout AM, Li R, Xiong J;

WPI; 2002-188687/24.

Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.

Claim 21; Page; 55pp; English.

The invention relates to a high affinity integrin polypeptide comprising

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call or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the Collb alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or CDID or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing reperfusion injury, immune complexes, restencis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in the printegrin alpha subunit CDID deletion variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847
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Sequence 177 AA;

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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                    CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                            Gaps
                                            ö
98.9%; Score 912; DB 5; Length 177; 98.3%; Pred. No. 2.6e-94; ive 2; Mismatches 1; Indels
                      Best Local Similarity 98.3
Matches 174; Conservative
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    Query Match
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AAY21991 standard; protein; 187 AA 13-SEP-1999 (first entry) AAY21991; RESULT 2 AAY21991 

Human complement factor MAC-1 vWF domain sequence.

Factor B analogue, modified, complement activity, complement factor B; short consensus repeat domain; von Willebrand Factor domain; human; C2; CR3; autoimmune response, tissue damage; lupus erythematosus; therapy; rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1; myocardial infarction; acute shock lung syndrome; inflammation; vWF.

Homo sapiens

US5928892-A.

27-JUL-1999

96US-00687706. 26-JUL-1996; 94US-00177109. 03-JAN-1994;

(UNIW ) UNIV WASHINGTON

Oglesby TJ, Hourcade DE;

WPI; 1999-429498/36.

Nucleic acids encoding complement protein homologues useful for modulating function of the complement system in the treatment of variety of immune and autoimmune complex mediated syndromes.

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Disclosure, Fig 5A-B, 53pp, English
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17-JUL-2002; 2002US-0396783P. L7-JUL-2003; 2003WO-US022301.

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complement activity in vitro. The analogue is generated by substituting a short consensus repeat domain (SCR) or a von Willebrand Factor domain (SCR) or a von Willebrand Factor domain as the consensus repeat domain (SCR) or a von Willebrand Factor domain as the consensus repeat domain (SCR) or a von Willebrand Factor domain as the bund of thuman C2 or CR3. The analogues may be used to regulate the complement system involved in immune and autoimmune responses. Complement activity can account for substantial tissue damage in a wide variety of autoimmune complex mediated syndromes such as lupus erythematosus, themmatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition of theumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition of therapeutic intervention in these cases. Inhibition of complement may also be favorable in cases that involve tissue damage caused by vascular caute shock lung syndrome. In these cases the complement system may contribute to the destruction, cerebral vascular accidents or acute shock lung syndrome. In these cases the complement system may contribute to the destruction, the use of complement system may contribute to the destruction, cerebral vascular accidents or reperfusion injury. In addition, the use of complement system may contribute to the destruction of partially damaged tissue as in novel target specificities could reduce the activity of tissue damaging proteins at sites of inflammation. Complement inhibition is important in the prevention of xenograft rejection (the inhibition of complement by cell-associated and soluble inhibitors is useful in protecting the transplant from damage caused by activation of endogenous complement. The present sequence represents the vWF domain of human factor MAC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant; osteopathic; cytostatic; immunosuppressive; antiinflammatory; europrotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thromboals; cancer; osteoporoals; signification sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EFONNPNPRSLVKPITTOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                       The invention relates to a Factor B analogue that exhibits modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.9%; Score 903; DB 2; Length 18
99.4%; Pred. No. 2.9e-93;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM99589 standard; protein; 1152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 187 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEFFFF
                                                                                                                                                                                                        The invention relates to a novel isolated or recombinant modified integrin protein having extracellular domains of integrin alpha and beta subunits where one of the subunits has one or more mutations, an altered surface feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-cysteine residue to cysteine or extracellular mutation that alters a non-cysteine residue to cysteine or extracellular comparison of integrin alpha and beta subunits. The polypeptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic, cytostatatic, immunosuppressive, antiinflammatory, neuroprotective and antisickling activities and may be useful for immunocherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple sclerosis. The current sequence is that of the human integrin alpham such an unitegrin alpham invention.
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                                                                                                                              Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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Pred. No. 3.7e-92;
0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by mRNA of the invention #45.
                                                                                                                                                                                   Disclosure; SEQ ID NO 4; 232pp; English
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17-JUL-2002; 2002US-0396790P.
11-SEP-2002; 2002US-0410135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2002; 2002US-00131831
                                      (BLOO-) CENT BLOOD RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.4
Matches 175; Conservative
                                                               Takagi J;
                                                                                         2004-122877/12.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1152 AA;
                                                                                                       N-PSDB; ADM99588
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                                                                Springer TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                         Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or tungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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                                                            Morris M;
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99.4%; Pred. No. 3.7e-92;
ive 0; Mismatches 1; Indels
                                                            Prentice J,
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non-specific defence system; integrin gene superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .16
/labal= signal_peptide
86. .88
-240. .242
/label= putative N-glycosylation site
/label= putative N-glycosylation site
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                                                            Ly N,
                                                                                                                                                                                                                                                                                                                                                                  Claim 65; SEQ ID NO 2444; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
(EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                         Woodward R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR04136 standard; protein; 1153
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nes 175; Conservative
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                                                         Wohlgemuth J, Fry K,
Rosenberg S;
                                                                                                                                                  WPI; 2004-400724/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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07-SEP-1990
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                                                                                                                                                                                                                                                                                                         the genes
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Modified-site

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Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating inflammation and viral infections, and in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 903; DB 2; Length 1153;
Pred. No. 3.7e-92;
0; Mismatches 1; Indels
                                                                                                     .abel= putative N-glycosylation site 102. .804
                                                                                                                           Label = putative N-glycosylation site 181. .883
                                                                                                                                                  Label= putative N-glycosylation site 101. 903
                                                                                                                                                                        .anel= putative N-glycosylation site 112. .914
                                                                                                                                                                                               /label= putative N-glycosylation site /label= putative N-glycosylation site /label= putative
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391. 393
/label= putative N-glycosylation site
469. 471
/label= putative N
                                 .abel= putative N-glycosylation site (593 . 695 . 1abel= putative ...
                                                                              /label= putative N-glycosylation site 735. .737
                                                                                                                                                                                                                                                                                                     14. .996
|abel= putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                               1045. .1047

label= putative N-glycosylation site

(1051. .1053

label= putative N-glycosylation site

1076. .1078

1106. .1134
                                                                                                                                                                                                                                                                             :l= putative N-glycosylation site .996
                                                                                                                                                                                                                                                                                                                                    label= putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                              /label= putative_transmembrane_region
                                                                                                                                                                                                                       / rabel = putative N-glycosylation 947. 949 / label = putative N-glycosylation
                                                       .....putative N-glycosylation 697. .699 putative N-glycosylation /label= putative
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Best Local Similarity 99.4%;
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening assay for modulators of integrin binding - using immobilised on labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                                                                                                                                                                                Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit;
                  EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                           DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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97.9%; Score 903; DB 2; Length 1153;
Best Local Similarity 99.4%; Pred. No. 3.7e-92;
Matches 175; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                      Human Beta-integrin CD11b subunit protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Fig 1A-D; 106pp; English.
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94US-00286889.
94US-00362652.
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                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis
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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60

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al Similarity 175; Conser

Query Match Best Local S: Matches 175

1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQ

264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFF 176

121

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셤 ò 셤 ò 셤 Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.

Human integrin 1 alpha-M subunit protein.

(first entry)

15-JUL-2002

AAU80252;

AAU80252 standard; protein; 1153

Misc-difference 499. .500 /note= "Encoded by GGG CAG AGG"

WO200218583-A2

07-MAR-2002

Springer TA, Shimoaka M, Lu C;

WPI:

Example 5; Fig 1; 270pp; English.

31-AUG-2001; 2001WO-US027227.

01-SEP-2000; 2000US-0229700P. (BLOO-) CENT BLOOD RES INC

Location/Qualifiers

Homo sapiens

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Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury sites.
                                                                                                                                                           263
                                         203
                                                                                                  EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adheaion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.
CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                        204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immosupersesive activities. The polypeptides of the invention have an open conformation and are useful simmunogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease, nephritis; human immunodeficiency virus (HIV), myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified integrin-I or integrin I-like domain polypeptide useful as a immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 109-112; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-382964/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK50046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conformation
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have an integrins. Leu-CAMS, leukcintegrins or beta2 subunit: the leukcoyde integrins. Leu-CAMS, leukcintegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence responsit is alpha d (AAA60014 and AAB07359). The present sequence has approximately 60% identity to the protein sequence of alpha d. The approximately 60% identity to the protein sequence of alpha d. The caberrant alpha d function eng. Type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory (LAD). In addition, anti-alpha d monoclomal antibodies may be used in the inflammation of macrophage infiltration at the site of a central nervous system injury. The monoclonal antibodies can also be used to detect and

diagnose Crohn's disease

Sequence 1153 AA,

selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor accovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphaD cobns and proteins, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the

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Length 1153; 1; Indels

97.9%; Score 903; DB 5; 99.4%; Pred. No. 3.7e-92; iive 0; Mismatches 1;

Best\_Local Similarity 99.4 Matches 175; Conservative

Query Match

Sequence 1153 AA;

61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120

204 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263

144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203

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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK

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Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integerin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin alpha M protein subunit used to generate the mutant
                                                                                                                                                                                                                                                                                                     204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                                                                                                                                                                                                                                                     EFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                      144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta2 integrin, alphaD subunit, CD11c subunit, CD11b subunit; LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis, arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease, Crohn's disease, ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; intracellular call adhesion molecule; vascular cell adhesion molecule; accometor recovery; locometor damage, locometor impairment; autonomic dysfunction; sensory dysfunction; spinal cord injury.
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                                                                                                                                                                                                                        CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSBEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                    DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                            Gaps
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                                                                                                                                                             Length 1153;
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                                                                                                                                                         Score 903; DB 5;
Pred. No. 3.7e-92;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Beta2 integrin alphaCD11b subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG61469 standard; protein; 1153 AA
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                                                                              integrin-1 alpha-M protein sub
polypeptides of the invention
                                                                                                                                                            97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002 (first entry)
                                                                                                                                                                                         Matches 175; Conservative
                                                                                                                                                                            Local Similarity
                                                                                                                               Sequence 1153 AA;
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open conformation; integrin related inflammatory disorder; integrin related immunological disorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New integrin I domain protein having alteration in at least 2 noncontiguous regions and exits in an open conformation, useful for treating, preventing or suppressing inflammatory or immunological disorders.
                                                264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CALY ) CALIFORNIA INST OF TECHNOLOGY (BLOO-) CENT BLOOD RES.
                                                                                                                                                                                                                                                                                                                                    AA014428 standard; protein; 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Integrin Mac-1 alpha subunit.
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The invention relates to promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dystunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin apphas subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand

Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.

WPI; 2002-463260/49.

Example 5; Page 191-194; 270pp; English.

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Ledbetter JA, Hayden-Ledbetter MS,
                                                                                                                                                                                                      ADD25615 standard; protein; 1153 AA
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                        25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                          (first entry)
                                                                                                             Best Local Similarity 77.3
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENECRAFT INC.
                                                                                                            Local Similarity
                                                                                              Sequence 1153 AA;
                                                                                                                                                                                                                                                                                                     US2003118592-A1
                                                                                                                                                                                                                                                                                           Unidentified.
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comparising a binding domain-immunoglobulin fusion protein comparising a binding domain polypeptide, an immunoglobulin heavy chain crownersing a binding domain polypeptide, an immunoglobulin heavy chain cross and a binding region polypeptide, and an immunoglobulin heavy chain crist constant region polypeptide that is fused to the CHZ constant region polypeptide that is fused to the CHZ constant region polypeptide. The mumoral constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comparises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comparises, where the first cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains contains a cysteine residues, where the first cysteine is not mutated; and a mutated human IgG1 immunoglobulin hinge region polypeptide contains or contains and a mutated human IgG1 immunoglobulin hinge region polypeptide contains or cysteine residues; where the first cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin fusion protein; a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein; a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein; a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein; a seconding the binding domain-immunoglobulin fusion protein or a polymucleotide and a carrier; and treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carrier, and insulpor and protein or polymucleoride and a carrier; and treating a binding domain-imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                    New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 97.9%; Score 903; DB 7; Length 11 al Similarity 99.4%; Pred. No. 3.7e-92; 175; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                          Disclosure; SEQ ID NO 176; 157pp; English
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Best Local Similarity
   WPI; 2003-801317/75.
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                                                                                                      domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises mucleic acids encoding the variant integrin I domain proteins. The integrin I domain proteins and nucleic acids are useful for treating. preventing or suppressing integrin related inflammatory and immunological glorders (e.g. rheumatoid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating, proteins and nucleic acids can also be used for treating ischaemia/ reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidabetic; antithyroid; neuroprotective; hinge region; famunoglobulin heavy chain; CH2 constant region; dimmunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antignition; Becal disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                      invention comprises structurally biased variant integrin inserted (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPRDHVFQVNNFE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain-immunoglobulin fusion protein-associated protein #85.
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                           Example 1; Fig 1F; 90pp; English.
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            Homo sapiens.
                       07-FEB-2002,
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or var residue 313 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemiant expertusion injury, immune complexes, restenosis and parasitic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-like domain; inflammactory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847
                                 /label= Gly, Ala
/note= "Wild-type Ile substituted by Gly or Ala"
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                                                                                                                                                                                                                                                                                                                                                        Human integrin alpha subunit CD11b variant A domain.
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                                                                                                                                                                                              AAU76856 standard; protein; 191 AA
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13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant conference at the subunit A-like domain. The polypeptide, preferably the confidence authority A-like domain. The polypeptide, preferably the confidence authority and A at residue 332 has been replaced by C or A residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or C or determining if a test compound is a candidate compound for binding to C D11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds CC to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemian reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b deletion variant A domain. Note: This variant sequence is not featured in the specification but has been constituted from the wild-type protein shown in AAU76847
                                                                                                       Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-11ke domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
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                                                  Human integrin alpha subunit CD11b deletion variant A domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Wild-type Phe substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type Ala substituted by
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Page; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnaout AM, Li R, Xiong J;
21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
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Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 177
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 17
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Gaps

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2; Indels

Length 191;

DB 5;

Score 893; DB 5; Pred. No. 4e-92; 2; Mismatches

96.98;

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61 EPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                             1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS
            integrin alpha subunit CD11b A domain
                                                      Query Match
Best Local Similarity 97.7
Warches 172; Conservative
                                       Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                     AAB66766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain. The polypeptide, preferably the CD11b alpha subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to determining if the test compound binds to the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemiareperfusion injury, immune complexes, restences and parasitic diseases, to purify variant integrin polypeptide ligands and as batt proteins in two-hybrid or three-hybrid assays. This sequence represents the human
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                                                                                                     EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                               Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-11ke domain; inflammatory disorder; skeletal muscle injury; restenos ischaemia-reperfusion injury; immue complex; parasitic disease; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
                                                                                                                     CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                 CPQEDSDIAFLIDGSGS11PHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                         DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                       Gaps
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    188
    /note= "This region is specifically claimed"

                         Indels
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            4e-92;
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                       Mismatches
           Pred. No.
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97.7%; Pre-
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11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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         Best Local Similarity 97.7
Matches 172; Conservative
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The present invention relates to generating a specific binding partner to a peptide, encoded by a genomic DNA fragment or an expressed sequence tag (EST). A nucleic acid molecule encoding a fusion protein is expressed in a host cell to allow the formation of inclusion bodies comprising the fusion protein, the inclusion bodies are isolated and a specific binding partner is generated. The specific binding partners generated are useful for identifying and characterizing naturally occurring proteins e.g. as immunoglobulins or fragments in immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic
61 EPQNNPNPRSLVKPITQLIGRTHIATGIRKVVRELFNITNGARKNAFKLLVVLTDGEKFG 120
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                                                                                   121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFF 176
                                                                                                                      121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating specific binding partners to (poly)peptides encoded by g
DNA fragments, involves forming inclusion bodies by expressing the
(poly)peptide as part of fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; inclusion body; binding partner;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of human CR-3 alpha chain and His tag.
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Pred. No. 1.4e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000WO-EP006137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-00112815
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Db 12 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN 71

Qy 66 PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGY 125

Db 72 PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGY 131

Qy 126 EDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176

Db 132 EDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 182

SGarch Completed: January 13, 2005, 15:12:33

Job time: 34.0928 86CS
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1
 LENGTH: 191
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Sequence 176, Appl
Sequence 6, Appli
Sequence 5, Appli
Sequence 4, Appli
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1 CPQEDSDIAFLIDGSGSIIP......NTIASKPPRDHVFQÇNNFEC 1<sup>1</sup>7
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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-945-265-4

US-09-945-265-3

US-09-902-481A-1

US-10-144-259-30

US-10-144-259-30

US-10-144-259-30

US-10-207-655-176

US-09-902-481A-6

US-09-902-481A-5

US-09-902-481A-4

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Sequence 9, Appli
Sequence 48, Appli
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Sequence 55, Appli
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Sequence 69, Appli
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Sequence 67, Appli
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Sequence 53, Appli
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US-10-362-812-5

US-09-902-481A-3

US-09-902-481A-3

US-09-350-259-101

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US-09-758-493-2
US-10-144-259-2
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US-09-350-259-4
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## ALIGNMENTS

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Sequence 1, Application US/09805354

Sequence 1, Application No. US20030078375A1

GENERAL INFORMATION:

APPLICANT: Armaout, M. Amin

APPLICANT: Atmout, M. Amin

APPLICANT: Almout, M. Amin

APPLICANT: Xiong, Jian-Ping

TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF

TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/805,354

CURRENT FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-01-11

PRIOR PELLOR TILING DATE: 2000-07-31

PRIOR PELLOR OFFE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PRECEDE OF Windows Version 4.0

SEQ ID NO 1.
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97.9%; Score 903; DB 10; Length 191;
Best Local Similarity 99.4%; Pred. No. 6.2e-89;
Matches 175; Conservative 0; Mismatches 1; Indels
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Sequence 4, Appli Sequence 17, Appl

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Best Local Similarity 99.4
Matches 175, Conservative
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ORGANISM: Homo sapiens
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DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                          DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 60/758,493
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                               Sequence 1, Application US/09758493

Sequence 1, Application No. US20040086935A1

GENERAL INFORMATION:
APPLICANT: Armout, M. Amin
APPLICANT: Armout, M. Amin
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 00786-804001
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0
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99.4%; Pred. No. 6.2e-89;
iive 0; Mismatches 1; Indels
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Matches 175; Conservative
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ORGANISM: Homo sapiens
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Sequence 4, Application US/09945265

Patent No. US20020123614A1

GENERAL INCORMATION:

APPLICANT: Springer, Timothy A.

APPLICANT: Shimaoka, Motomu

APPLICANT: Shimaoka, Motomu

APPLICANT: Lu, Chafen

TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME

FILE REFERENCE: CBN-002CP

CURRENT APPLICATION NUMBER: US/09/945,265

CURRENT FILING DATE: 2001-08-31

PRIOR PILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 4

SSOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
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                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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Patent No. US2002062008A1
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20020062008A1el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1998-01-08
EARLIER PEPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/193,497
EARLIER APPLICATION NUMBER: 08/13,497
EARLIER PILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/36,652
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99.4%; Pred. No. 7.3e-88;
tive 0; Mismatches 1;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT'S GALIBATION, Michael W.
APPLICANT'S GALIBATION, Michael W.
APPLICANT'S GALIBATION, Michael W.
TITLE CAMT'S UNDER VIENCEN, MONICA
TITLE OF INVENTION: NO. US20030077278Alel Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT PLING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR PLING DATE: 1994-108-05
PRIOR PLING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR PRILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PAECHLIN VOWER: 08/943,363
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PAECHLIN VOYE: 2.0
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Best Local Similarity 99.4%;
Matches 175; Conservative (
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CRGANISM: Homo sapiens
US-10-144-259-30
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO
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                                                                                                                                                                                                                       Query Match 97.9%; Score 903; DB 9; Length 1153; Best Local Similarity 99.4%; Pred. No. 7.4e-88; Matches 175; Conservative 0; Mismatches 1; Indels
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       EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1153
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Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-350-259-3
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NAME/KEY: mat_peptide
LOCATION: (17)..()
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US-09-902-481A-1
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US-09-902-481A-1
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US-09-891-943-3
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                                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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                                                                                                                                                                                                                                                                                                                                              DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Liong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
TILE REFERENCE: 00706-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 1153
                                                               0; Gaps
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Score 903; DB 10; Length 1153;
Pred. No. 7.4e-88;
0; Mismatches 1; Indels 0
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Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1;
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; Sequence 3, Application US/09891943

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TYPE: PRT
ORGANISM: Artificial sequence
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SOFTWARE: PatentIn version 3.1
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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                         204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                                      121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                264 DPLGYEDVIPEADREGVIRYVIGYGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-INWUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NOWER: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20030054440A1
Publication No. US20030054440A1
Publication No. US20030054440A1
APPLICANT: Springer, Timothy
APPLICANT: Shimmacka, Motomu
APPLICANT: Shimmacka, Mulia
APPLICANT: Shimmacka, Mulia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-207-655-176
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Best Local Similarity
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US-10-207-655-176
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LENGTH: 1137
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US-09-902-481A-6
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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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APPLICANT: Springer, Timothy
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RT/RMS/RMK
CURRENT PILING DATE: 2001-07-09
PRIOR PELICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
IENGTH: 1137
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APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Mayo, Stephen
TTLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: U5/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
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Best Local Similarity 95.5%; Pred. No. 2.3e-86;
Matches 168; Conservative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION:
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65 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
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95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels
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Pred. No. 3.9e-86;
0; Mismatches 1;
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Sequence 9, Application US/10615515
Publication No. US20040132974A1
GENERAL INFORMATION:
APPLICANT: FAGAN, RICHARD, JOSEPH
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575_2004
CURRENT APPLICATION NUMBER: US/10/615,515
CURRENT FILING DATE: 2003-07-08
FRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: GB 0100750.9
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: GB 0100750.9
PRIOR FILING DATE: 2001-01-11
SEQIENT ON SEQIEN NOS: 12
SOFTWARE: PATCHIN VOS: 12
SEQIEN NO 9
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GUTTERLOGE, ALEX
TILE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 37
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Best Local Similarity 99.4%;
Matches 171; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-346-863-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EFQNNPNPPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 EFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLLTDGEKFG 247
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95.3%; Score 879; DB 10;
Best Local Similarity 94.9%; Pred. No. 2.8e-85;
Matches 167; Conservative 6; Mismatches 3;
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Pred. No. 3.8e-86;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GS-10-346-803-17, Application US/10346863
Publication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GTTERINGE, ALEX
TITLE OF INVERTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT APPLICATION NUMBER: PCT/0801/0318
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR PLILING DATE: 2000-07-24
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Publication No. US20040038325A1
GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 171; Conservative (
                                                                          TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                 , OTHER INFORMATION: synthetic US-09-902-481A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-17
         SEQ ID NO 4
LENGTH: 1137
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LENGTH: 184
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125 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176

Search completed: January 13, 2005, 15:39:45 Job time : 30.2475 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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Pred. No. 8.9e-93;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent no. 5865015
; GENERAL INFORMATION:
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patera L. Pabet
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Babst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCY/DOCKET NUMBER: WI 107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (404) 873-8794
TELEFRAX: (404) 873-8795
INFORMATION POR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LRNGTH: 187 amino acids
US-08-605-672-37
US-08-482-293A-37
US-08-193-363-37
US-09-193-043-37
US-09-180-259-37
US-08-485-618-55
US-08-485-618-55
US-08-943-363-55
US-08-943-363-55
US-09-193-043-55
US-09-193-043-55
US-09-193-043-55
US-09-183-048-55
US-08-173-497-2
US-08-173-497-2
US-08-185-618-2
US-08-185-618-2
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Best Local Similarity 99.4
Matches 175; Conservative
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HYPOTHETICAL: NO
US-08-177-109A-61
      linear
      TOPOLOGY:
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Sequence 101, App
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Sequence 101, App
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Sequence 101, App
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
                                                                                                                                                                                                           January 13, 2005, 15:07:42 ; Search time 8.50625 Seconds (without alignments) 1379.959 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-687-706-61

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US-08-176-062A-13

PCT-US56-01314-43

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US-08-186-889-3

US-08-186-18-3

US-08-185-18-3

US-08-185-13-3

US-08-185-13-3

US-08-185-13-3

US-08-185-13-3

US-09-193-04-3

US-09-185-1101

US-08-185-1101

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Score

Result No.

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GENERAL INFORMATION: APPLICANT: Arnaou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEFRIHFTFK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHFTFK
                                                                                          121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPRDHVFQVNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPLGYEDVI PEADREGVIRYVI GVGDAFRSEKSROELNTI ASKPRDHVFOVNNFE 176
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                                                                                                                                                                                                        Sequence 61, Application US/08687706
Patent No. 5928892
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby TITLE OF INVENTION:
MUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARTS TITES (CONTROLL) (SOFTWARTS PATENTIAL STATES APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26-UUL-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIE: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-476-062A-43
; Sequence 43, Application US/08476062A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 187 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO US-08-687-706-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                               RESULT 2
US-08-687-706-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: ADDRESSE: Fish For Support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1152;
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TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 18-JUN-1980
APPLICATION NUMBER: 07/212,573
FILING DATE: 18-JUN-1981
ATTORNEY-AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 903; DB 2;
Pred. No. 1e-91;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00786/068003
                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-01314-43; Sequence 43, Application PC/TUS9601314; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               CILL
STATE: MA
COUNTRY: US
TO 02110-2804
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BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1474-6300
TELEFRAX: 312-474-6300
                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08173497
Patent No. 5437958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.4
Matches 175; Conservative
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                      US-08-173-497-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATEGIT NO. 5424399

PAPLICANT: ARNAOUT, M. AMIN

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FILING DATE: 16-JUN-1993

PRIOR APPLICATION NUMBER: 539,842

FILING DATE: 18-JUN-1990

PRILING DATE: 18-JUN-1990

PRILING DATE: 28-JUN-1990

FILING DATE: 28-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 903; DB 6;
Pred. No. 1e-91;
0; Mismatches
                                                                                      COUNTRY: U.S.A.

ZIP: 0110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
PRING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
PRILNG DATE: 30-JAN-96
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTONNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE: (617) 542-8906
ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%;
99.4%;
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Best Local Similarity 99.44
Matches 175, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                  Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1152
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, LENGTH: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
PCT-US96-01314-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5424399-2
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204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                                                                                                                                             144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                               61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                             1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                         121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 903; DB 1; Length 1153; 99.4%; Pred. No. 1e-91; tive 0; Mismatches 1; Indels
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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60

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Illinois
: United States
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STRANDEDNESS: sin
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                                                                   60606-6402
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US-08-362-652-3
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                Sequence 3, Application US/08286889
Pacent No. 5470953
CENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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97.9%; Score 903; DB 1; Length 1153;
Best Local Similarity 99.4%; Pred. No. 1e-91;
Matches 175; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                          CUNTRY: United States
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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                                                                                                                                                                                                                                              CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
US-08-286-889-3
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 903; DB 1; Length 1153; 99.4%; Pred. No. 1e-91; Live 0; Mismatches 1; Indels (
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
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COMPUTER: PACHOLISH FORM:
COMPUTER: PACHOLISH FORM:
APPLICATION NUMBER: US/08/485,618
FILING DATE: 23-DEC-1993
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
FILING DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
MAPPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTOMNEY/AGENT INFORMATION:
ANAME: ALL DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/POCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
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COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.4
Matches 175; Conservative
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COMPUTER READABLE FORM:
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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Sequence 3, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 903; DB 2; Length 1153;
Pred. No. 1e-91;
0; Mismatches 1; Indels
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CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
                                       PILING DATE: 23-DEC-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGRYT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAKE: 312-474-6300
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TELERAX: 312-4/1.
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
STANTH: 1153 amino acids
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.4%;
Matches 175; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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US-08-482-293A-3
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Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                     COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                      27866/32391
                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTATION NUMBER: 338,659
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FILING DATE:
                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,655
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION: 312-474-6300
TELEFAX: 312-474-0448
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1153 amino acids
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
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                                                                                                                                                      FILING DATE:
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Query Match 97.9%;
Best Local Similarity 99.4%;
Matches 175; Conservative
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                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-943-363-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                     amino acid
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Patent No. 5837478
GENERAL INFORMATION:
GENERAL INFORMATION:
M. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
I14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                   NAME: /williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        TELEFAX: 312-7.
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
5-AUG-1994
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CLASSIFICATION:
FILING DATE:
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Pred. No. 1e-91;
0; Mismatches 1; Indels
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILLE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PELLOATION NUMBER: 08/173,497
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTY OFF: 2.0
                                                                    27866/32684
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NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                             REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEINTIASKPPRDHVFQVNNFE 319
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                                                                                                                                                                                                                                                                              APPLICANT: Galiatin, Michael W.
APPLICANT: Galiatin, Michael W.
ITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REPERSENE: 27866/3646
GURENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR PILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/343,363
PRIOR PILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/343,363
PRIOR APPLICATION NUMBER: 08/343,363
PRIOR PILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIN Ver: 2.0
SEQ ID NO 3
LENGTH: 1153
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Sequence 3, Application US/09350259
Fatent No. 6620915
GENERAL INPORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6620915el Human 2:
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER PELING DATE: 1998-11-16
EARLIER PEPLICATION NUMBER: 08/173,497
EARLIER PEPLICATION NUMBER: 08/173,497
EARLIER PEPLICATION NUMBER: 08/265
EARLIER PEPLICATION NUMBER: 08/36,652
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
                                                                                                                                                                     Sequence 3, Application US/09688307A Patent No. 6432404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  APPLICANT: Gallatin, Michael W.
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Best Local Similarity 99.4
Matches 175, Conservative
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US-09-688-307A-3
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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Pred. No. 1e-91;
0; Mismatches 1
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Job time: 9.50625 secs
                                                                                                                                                                                                    97.98;
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4
Matches 175; Conservative
                                                                    ; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3
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